

GenCore version 5.1.3
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UM protein - protein search, using sw model

Run on: January 28, 2003, 11:43:11, Search time 39 Seconds
(without alignments)
1387.173 Million cell updates/sec

Title: US-09-828-432-3

Perfect score: 2167

Sequence: 1 MNVFAHLHPAGGVLPSDSQ... QNNDPIPWHEDEGTGEGVK 406

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DR seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A_Geneseq_101002.*

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12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
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20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
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22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2167	100.0	406	AAU98047	Human HGRPMY7 N-t
2	2167	100.0	406	AAU98048	Human HGRPMY7 C-t
3	2167	100.0	406	AG361638	Human G-protein-co
4	2167	100.0	406	AAU10631	Novel G-protein-co
5	2167	100.0	419	AAU08807	Galanin receptor-1
6	2167	100.0	419	AAE06761	Human G-protein co
7	2167	100.0	419	AAE06344	Amino acid sequenc
8	2167	100.0	419	AAU04363	Human G-protein co
9	2167	100.0	419	AAU01848	Human DNA G-protei
10	2167	100.0	419	AAE06091	Human G-protein-co

11	2167	100.0	419	23	AAU10630	Novel G-protein co
12	2167	100.0	419	23	AAE17882	Human G-protein co
13	2164	99.9	419	22	AAAG63345	Amino acid sequenc
14	2164	99.9	419	22	AAAG64120	Human G-protein-co
15	2162	99.8	418	22	AAU73244	Human fetal brain G
16	2055	94.8	461	23	AAU97909	Human 52874 G prot
17	916	43.2	237	22	AAU25623	G protein coupled
18	588	27.6	110	23	ABG61646	Human G-protein-co
19	270.5	12.5	371	19	AAW61463	Mouse galanin rece
20	270.5	12.5	371	19	AAW61388	Mouse galanin rece
21	270.5	12.5	371	19	AAW49004	Mouse galanin rece
22	270.5	12.5	371	23	AAU74549	Mouse galanin rece
23	269.5	12.4	346	20	AAU74512	Human 52874 G prot
24	269.5	12.4	346	22	AAE05138	Rat galanin recept
25	269.5	12.4	346	23	AAAG68218	Rat galanin recept
26	268	12.4	372	19	AAW40135	Rat GalR2 receptor
27	267	12.3	372	18	AAW24561	Rat galanin recept
28	267	12.3	372	19	AAW61385	Rat galanin recept
29	267	12.3	372	19	AAW49002	Rat galanin recept
30	267	12.3	372	19	AAW61461	Rat galanin recept
31	267	12.3	372	19	AAW62251	Rat galanin recept
32	267	12.3	372	19	AAW40136	Rat GalR2 receptor
33	267	12.3	372	20	AAU45130	Rat galanin recept
34	267	12.3	372	22	AAE65139	Rat galanin recept
35	267	12.3	372	23	AAU74547	Rat galanin recept
36	267	12.3	372	23	AAAG68219	Rat galanin recept
37	265.5	12.3	368	20	AAU06519	Human galanin rece
38	265	12.2	385	19	AAW52252	Human galanin rece
39	265	12.2	387	18	AAW4562	Human galanin rece
40	265	12.2	387	19	AAW61462	Human galanin rece
41	265	12.2	387	19	AAW61386	Human galanin rece
42	265	12.2	387	19	AAW49003	Human galanin rece
43	265	12.2	387	23	AAU74548	Human galanin rece
44	264	12.2	348	17	AAU95069	Mouse pancreas bet
45	264	12.2	348	17	AAU91229	Mouse pancreas 3-p

ALIGNMENTS

RESULT 1
AAU98047
ID AAU98047 standard; Protein; 406 AA.
XX AAU98047;
XX
DT 13-AUG-2002 (first entry)
XX
DE Human HGRPMY7 N-terminal deletion mutant representative sequence.
XX
KW Human; G-protein-coupled receptor; HGRPMY7; spinal chord;
KW spinal chord-related disorder; breast cancer; neoplastic disease;
KW brain disorder; leukaemia; myeloma; immunological disorder;
KW cholecystitis; Grave's disease; osteoarthritis; asthma;
KW neurological disorder; dementia; Alzheimer's disease;
KW Down's syndrome; epilepsy; intracellular calcium level; NFAT;
KW nuclear factor activator of transcription element; mutant; mutein.
XX
OS Homo sapiens.
XX Synthetic.

Key Location/Qualifiers

FT Misc-difference 1..399

/note="The N-terminus can be officially and sequentially deleted by one amino acid at a time"

XX WC200226823-A2.

XX 04-APR-2002.

XX 26-SEP-2001; 2001WC-US30351.

XX 27-SEP-2000; 2000US-235731P.

PP 14-SEP-2001; 2001US-268580P.
PP 28 AUG 2001; 2001US-315423P.
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX Battaglino P, Feder JN, Mintier G, Ramanathan CP, Westphal P;
PI Hawken DR, Cacace A, Barber L, Kornacker MG;
XX WPI; 2002-435195/46
XX Novel human G protein coupled receptor RMY7 (HGPRMY7) polypeptide,
PT useful for modulators of HGPRMY7 activity that are useful for treating
PT leukaemia, cholecystitis, Grave's disease, epilepsy, dementia,
PT depression -
XX Claim 12; Fig 2; 170pp; English.
XX The invention relates to an isolated polypeptide (I) comprising amino
CC acid sequence that is at least 95% identical to a polypeptide fragment of
CC a fully defined human G protein-coupled receptor RMY7 (HGPRMY7).
CC Polypeptide, or variant, allelic variant or species homologue.
CC Also included are polynucleotides encoding the above polypeptides,
CC expression vectors, host cells, anti-HGPRMY7 antibodies and modulators
CC of HGPRMY7. HGPRMY7 and its polynucleotide are useful for diagnosis
CC prevention, treating or ameliorating a medical condition e.g. a disease,
CC disorder, or a condition related to brain, breast, gastrointestinal or
CC musculo-skeletal systems, such that thalamus, corpus callosum,
CC cerebellum, caudate nucleus, amygdala, substantia nigra,
CC hippocampus, brain, breast, colon, spinal chord-related disorders,
CC breast cancer, neoplastic diseases, and disorders related to spinal
CC chord and brain. An antagonist or inhibitor of (I) identified using (I)
CC is useful for treating a neoplastic disorder such as leukaemia, myeloma,
CC immunological disorders such as cholecystitis, Grave's disease,
CC osteoarthritis, asthma, neurological disorders such as dementia,
CC depression, Alzheimer's disease, Down's syndrome and epilepsy.
CC HGPRMY7, its polynucleotide and agonists or antagonists of the
CC modulating Ca²⁺ sensitive signalling pathways and modulating nuclear
CC factor activator of transcription (NFAT) element associated signalling
CC pathways. The present sequence is a representative sequence for a
CC set of sequential N-terminal deletion mutants of HGPRMY7.
XX SQ Sequence 406 AA;
Query Match 100.0%; Score 2167; DB 23; Length 406;
Best Local Similarity 100.0%; Pred No. 2 5e 191;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNVSFAHLHPAGGYIPSDQCTWPTITALLVAVCVGVYQNIQVIGITLLNNAWKYPSPMI 60
DB 1 MNVSFAHLHPAGGYIPSDQCTWPTITALLVAVCVGVYQNIQVIGITLLNNAWKYPSPMI 60
QY 61 HSLILNLGLADIALLPSAPIPATATSKSVMDLGMVCKSSDWFHTCMAAKSLTIIVVA 120
DB 61 HSLILNLGLADIALLPSAPIPATATSKSVMDLGMVCKSSDWFHTCMAAKSLTIIVVA 120
QY 121 FVCFVYVASSPAKGVSHNNTIMVVLVAVIMTVASLLPLFEPFSTPIPHREGVMLVDVFA 180
DB 121 FVCFVYVASSPAKGVSHNNTIMVVLVAVIMTVASLLPLFEPFSTPIPHREGVMLVDVFA 180
QY 181 VAEEMFMKFNPLAAGLPLFASFYFYPAYCTQYFSTTQHLPRNIRKQVTVML 240
DB 181 VAEEMFMKFNPLAAGLPLFASFYFYPAYCTQYFSTTQHLPRNIRKQVTVML 240
QY 241 STAIISALLLPEWAWLWWHLKAAGPAPPGCFIALSQVLFSSISSANPLIFLWMSSEF 300
DB 241 STAIISALLLPEWAWLWWHLKAAGPAPPGCFIALSQVLFSSISSANPLIFLWMSSEF 300
QY 301 PCLKGVWMMITVPTVSEGETAPKNSGIPVVPVPEFSPASIPKEXPSRSSQV 360
DB 301 PCLKGVWMMITVPTVSEGETAPKNSGIPVVPVPEFSPASIPKEXPSRSSQV 360
QY 361 KTEKAPILPVDFQFQWHPEDTVFVSQNDPIPWFHEHDETQETV 406

EB 361 KTEKAPILPVDFQFQWHPEDTVFVSQNDPIPWFHEHDETQETV 406
RESULT 2
AAU98048
ID AAU98048 standard; Protein; 406 AA.
XX AC AAU98048;
XX 13-AUG-2002 (first entry)
XX Human HGPRMY7 C-terminal deletion mutant represent at two sequences.
XX Human; G protein-coupled receptor; HGPRMY7; spinal chord;
KW spinal chord-related disorder; breast cancer; neoplastic disease;
KW brain disorder; leukaemia; myeloma; immunological disorders;
KW cholecystitis; Grave's disease; osteoarthritis; asthma;
KW neurological disorder; dementia; depression; Alzheimer's disease;
KW Down's syndrome; epilepsy; intracellular calcium levels; NFAT;
KW nuclear factor activator of transcription element; mutant; modulator.
XX Homo sapiens.
XX Synthetic.
XX Key Location/Qualifiers
XX Misc-difference 8:1-406 /notes "The C-terminus can be optionally and sequentially
XX deleted by one amino acid at a time"
W0000226823 A2
04-APR-2002.
26-SEP-2001; 2001WO-US30351.
27-SEP-2000; 2000US-235731P.
14 FEB 2001; 2001US-268580P.
28-AUG-2001; 2001US-315423P.
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX Battaglino P, Feder JN, Mintier G, Ramanathan CP, Westphal P;
PI Hawken DR, Cacace A, Barber L, Kornacker MG;
XX WPI; 2002-435195/46.
XX Novel human G-protein coupled receptor RMY7 (HGPRMY7) polypeptide,
PT useful for modulators of HGPRMY7 activity that are useful for treating
PT leukaemia, cholecystitis, Grave's disease, epilepsy, dementia,
PT depression -
XX Claim 12; Fig 2; 170pp; English.
XX The invention relates to an isolated polypeptide (I) comprising amino
CC acid sequence that is at least 95% identical to a polypeptide fragment of
CC a fully defined human G protein-coupled receptor RMY7 (HGPRMY7).
CC Polypeptide, or variant, allelic variant or species homologue.
CC Also included are polynucleotides encoding the above polypeptides,
CC expression vectors, host cells, anti-HGPRMY7 antibodies and modulators
CC of HGPRMY7. HGPRMY7 and its polynucleotide are useful for diagnosis
CC prevention, treating or ameliorating a medical condition such as a disease,
CC disorder, or a condition related to brain, breast, gastrointestinal or
CC musculo-skeletal systems, such that thalamus, corpus callosum,
CC cerebellum, caudate nucleus, amygdala, substantia nigra,
CC hippocampus, brain, breast, colon, spinal chord-related disorders,
CC breast cancer, neoplastic diseases, and disorders related to spinal
CC chord and brain. An antagonist or inhibitor of (I) identified using (I)
CC is useful for treating a neoplastic disorder such as leukaemia, myeloma,
CC immunological disorders such as cholecystitis, Grave's disease,
CC osteoarthritis, asthma, neurological disorders such as dementia,
CC depression, Alzheimer's disease, Down's syndrome and epilepsy.
CC HGPRMY7, its polynucleotide and agonists or antagonists of the

CC polypeptide are useful for modulating intracellular calcium levels,
 CC modulating Ca²⁺ sensitive signalling pathways and modulating nuclear
 CC factor activator of transcription (NFAT) element associated signalling
 CC pathways. The present sequence is a representative sequence for a
 CC set of sequential C-terminal deletion mutants of HGPBMY7.

XX Sequence 406 AA,
 SQ

Query Match 100.0%; Score 2167; DB 23; Length 406;
 Best Local Similarity 100.0%; Pred. No. 2.5e-191;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNVSPAHLPAGGYLPSDSQDWRTIIPALLVAVCLVGFVGNLCVIGILLHNAWKGPMSI 60
 DB 1 MNVSPAHLPAGGYLPSDSQDWRTIIPALLVAVCLVGFVGNLCVIGILLHNAWKGPMSI 60
 QY 61 HCLILMLCAELSLFLSAPIRATAYSKSVWDLGFWCKSSDWFIHTCMAKSLTIIVVA 120
 DB 61 HSLILNLADLSLLFLSAPIRATAYSKSVWDLGFWCKSSDWFIHTCMAKSLTIIVVA 120
 QY 121 KVCFMASDPKQVSHNYITVNSVLAIVTWASLLPLPEWFFSTIRHHEGVEMCLVDVPA 180
 DB 121 KVCFMASDPKQVSHNYITVNSVLAIVTWASLLPLPEWFFSTIRHHEGVEMCLVDVPA 180
 QY 191 VAEFMSMFKLPLAFGLPLFPASFPWPDYDQCKKPGTKTQNLNPIRSQVTVMLL 240
 DB 181 VAEFMSMFKLPLAFGLPLFPASFPWPDYDQCKKPGTKTQNLNPIRSQVTVMLL 240
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 DB 241 SIALLSALLPFWAWLWWHLKAAGPAPQGFIALSQVLMFSISSANPLIFLVMSEEP 300
 QY 301 REGLGKGVWMMITTKPPTVSESQETPAGNSEGLPDKVPSPESPASIPETKEKPSSSSGKG 360
 DB 301 REGLGKGVWMMITTKPPTVSESQETPAGNSEGLPDKVPSPESPASIPETKEKPSSSSGKG 360
 QY 361 KTEKAEIPLPDVEQFWHERDTPVSVQDNDPIPWEHEDQETGEGVK 406
 DB 361 KTEKAEIPLPDVEQFWHERDTPVSVQDNDPIPWEHEDQETGEGVK 406

RESULT 3
 ABG61638
 ID AR61638 standard; Protein, 406 AA.
 AC ABG61638;
 XX

DT 13-AUG-2002 (first entry)

DE Humar G protein-coupled receptor HGPBMY7.

XX Human, G protein-coupled receptor, HGPBMY7, spinal chord,
 KW spinal chord-related disorder; breast cancer; neoplastic disease;
 KW brain disorder; leukaemia; myeloma; immunological disorder;
 KW cholecystitis; Grave's disease; osteoarthritis; asthma;
 KW neuropsychological disorder; dementia; depression; Alzheimer's disease,
 KW Down's syndrome; epilepsy; intracellular calcium level; NFAT;
 KW nuclear factor activator of transcription element.

XX Homo sapiens.

XX WC000026923-A2.

XX 04 APR 2002.

XX 26-SEP-2001, 2001WU (3/3/01)

XX 27-SEP 2000; 2000US-236731P.

XX 14-FEB-2001; 2001US-268580P.

XX 28-AUG 2001; 2001US-315423P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

PI

PI Battaglino P, Feder JN, Mintier G, Ramanathan CS, Westphal R;

XX Hawken DR, Cacace A, Barber L, Kornacker MG;

DR WP1; 2002-435195/46.

DR N-PSDR; ABK84809.

XX Novel human G-protein coupled receptor BMV7 (HGPBMY7) polypeptide.

PT useful for modulators of HGPBMY7 activity that are useful for treating

PT leukaemia, cholecystitis, Grave's disease, epilepsy, dementia,

XX depression -

PS Claim 11; Fig 2; 170pp; English.

XX The invention relates to an isolated polypeptide (1) comprising amino
 CC acid sequence that is at least 95% identical to a polypeptide fragment of
 CC a fully defined human G protein-coupled receptor BMV7 (HGPBMY7)

CC polypeptide, or variant, allelic variant or species homologue.

CC Also included are polynucleotides encoding the above polypeptides,

CC expression vectors, host cells, anti-HGPBMY7 antibodies and modulators

CC of HGPBMY7. HGPBMY7 and its polynucleotide are useful for diagnosis

CC prevention, treating or ameliorating a medical condition e.g. a disease,

CC disorder, or a condition related to brain, breast, gastrointestinal or

CC musculo-skeletal systems, such that thalamus-, corpus callosum-,

CC hippocampus-, caudate nucleus-, amygdala-, substantia nigra-,

CC cerebellum-, brain-, breast-, colon-, spinal chord-related disorders,

CC breast cancer, neoplastic diseases, and disorders related to spinal

CC chord and brain. An antagonist or inhibitor of (1) identified using (1)

CC is useful for treating a neoplastic disorder such as leukaemia, myeloma,

CC immunological disorders such as cholecystitis, Grave's disease,

CC osteoarthritis, asthma, neurological disorders such as dementia,

CC depression, Alzheimer's disease, Down's syndrome and epilepsy.

CC HGPBMY7, its polynucleotide and agonists or antagonists of the

CC polypeptide are useful for modulating intracellular calcium levels,

CC modulating Ca²⁺ sensitive signalling pathways and modulating nuclear

CC factor activator of transcription (NFAT) element associated signalling

CC pathways. The present sequence is the HGPBMY7 protein sequence.

XX Sequence 406 AA;

SQ Query Match 100.0%; Score 2167; DB 23; Length 406;

Best Local Similarity 100.0%; Pred. No. 2.5e-191;

Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNVSPAHLPAGGYLPSDSQDWRTIIPALLVAVCLVGFVGNLCVIGILLHNAWKGPMSI 60

DB 1 MNVSPAHLPAGGYLPSDSQDWRTIIPALLVAVCLVGFVGNLCVIGILLHNAWKGPMSI 60

QY 61 HSLILNLADLSLLFLSAPIRATAYSKSVWDLGFWCKSSDWFIHTCMAKSLTIIVVA 120

DB 61 HSLILNLADLSLLFLSAPIRATAYSKSVWDLGFWCKSSDWFIHTCMAKSLTIIVVA 120

QY 121 KVCFMASDPKQVSHNYITVNSVLAIVTWASLLPLPEWFFSTIRHHEGVEMCLVDVPA 180

DB 121 KVCFMASDPKQVSHNYITVNSVLAIVTWASLLPLPEWFFSTIRHHEGVEMCLVDVPA 180

QY 181 VAEFMSMFKLPLAFGLPLFPASFPWPDYDQCKKPGTKTQNLNPIRSQVTVMLL 240

DB 181 VAEFMSMFKLPLAFGLPLFPASFPWPDYDQCKKPGTKTQNLNPIRSQVTVMLL 240

QY 241 SIALLSALLPFWAWLWWHLKAAGPAPQGFIALSQVLMFSISSANPLIFLVMSEEP 300

DB 241 SIALLSALLPFWAWLWWHLKAAGPAPQGFIALSQVLMFSISSANPLIFLVMSEEP 300

QY 301 REGLGKGVWMMITTKPPTVSESQETPAGNSEGLPDKVPSPESPASIPETKEKPSSSSGKG 360

DB 301 REGLGKGVWMMITTKPPTVSESQETPAGNSEGLPDKVPSPESPASIPETKEKPSSSSGKG 360

QY 361 KTEKAEIPLPDVEQFWHERDTPVSVQDNDPIPWEHEDQETGEGVK 406

DB 361 KTEKAEIPLPDVEQFWHERDTPVSVQDNDPIPWEHEDQETGEGVK 406

RESULT 4


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PF 15-MAP-2001; 2001WO-EP02925
XX
XX 16-MAP-2000; 2000US-01P0999
PP 17-JUN-2000; 2000US-0210983
PR 07-DEC-2000; 2000US-0251515.
PA (FAPB ) RAYER AG.
XX
XX Pamakrishnan S;
PI
XX
XX WPI; 2001-582449/65
DP N PSDB; AAS13700.
DR
XX
XX Reagent and methods of regulating a galanin receptor-like G protein
PT coupled receptors and their regulation for therapeutic purposes e.g.
PT treatment of hypertension and asthma -
XX
XX Claim 1; Fig 2; 123pp; English.
XX
XX The invention describes novel reagents and methods of regulating a
CC galanin receptor-like G-protein coupled receptor for therapeutic
CC purposes, useful for treating disease by gene therapy. A pharmaceutical
CC composition described in the specification is useful for modulating the
CC activity of the Galanin receptor-like GPCR in a pathophysiological
CC disorder, selected from obesity, diabetes, cardiovascular disease,
CC asthma, pain, depression, ischaemia, Alzheimer's disease, sleep disorder,
CC migraine, anxiety and reproductive disorder. Specifically, the
CC composition is useful for modulating the activity of the receptor in
CC cognition, analgesia, sensory processing, processing or visceral
CC information, motor coordination, modulation of dopaminergic activity and
CC neuroendocrine function. This sequence is the Galanin receptor-like
CC G protein coupled receptor described in the method of the invention.
XX
XX G protein coupled receptor described in the method of the invention.
XX
XX Sequence 419 AA;
SQ
Query Match 100 0%, Score 2167, DB 22; Length 419;
Best Local Similarity 100 0%; Pred No. 2 6e-191;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MNVSPFAHLHPAGGYLPDSQGFHTIIPALLVAVCLVGFVGNLCVIGILLHNAWKGPMSI 60
DB 14 MNVSPFAHLHPAGGYLPDSQGFHTIIPALLVAVCLVGFVGNLCVIGILLHNAWKGPMSI 73
OY 61 HSLILNLSLADISSLFSAPIRATAYSKSVMDLGMFVCKSSDWFIHTCMAAKSLTIIVVVA 120
DB 74 HSLILNLSLADISSLFSAPIRATAYSKSVMDLGMFVCKSSDWFIHTCMAAKSLTIIVVVA 133
OY 121 KVCFMVYASDPKQVSHNNTYINSVLVAIWTVASLLPLPEWFFSTIRHHGVEMLVDVPA 180
DB 134 KVCFMVYASDPKQVSHNNTYINSVLVAIWTVASLLPLPEWFFSTIRHHGVEMLVDVPA 193
OY 181 VAEERMSMFRTYLPILAPLPIFPASFPWPAYTCYKFGTKTQNLRWDIRSKQVTVMLL 240
DB 194 VAEERMSMFRTYLPILAPLPIFPASFPWPAYTCYKFGTKTQNLRWDIRSKQVTVMLL 253
OY 241 STAITALLLPEWVAWLWWHLKAAGPAPPQGFIALSQVLMFSSANPLFLVWSEEF 300
DB 254 STAITALLLPEWVAWLWWHLKAAGPAPPQGFIALSQVLMFSSANPLFLVWSEEF 313
OY 301 PEGLCVAKVWMTTKPTVTSQETPAGNSEGLPKVPSPEPASIPKEKSPSSSGKG 360
DB 314 PEGLCVAKVWMTTKPTVTSQETPAGNSEGLPKVPSPEPASIPKEKSPSSSGKG 373
OY 361 KTEKAPILPDVQEQWHEHEDTVPSVQNDPIPWHEHEDQETGEGVK 406
DB 374 KTEKAPILPDVQEQWHEHEDTVPSVQNDPIPWHEHEDQETGEGVK 419
RESULT 6
ID AAE06761
XX AAE06761 standard; Protein, 419 AA
XX
XX AAE06761;

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16-OCT-2001 (first entry)

Human G-protein coupled receptor-11 (GCRC-11) protein.

Human: G-protein coupled receptor-11; GCRC-11; cytosolic; hepatotropic; virucide; antiinflammatory; anticonvulsant; antiemetic; neuroprotective; nootropic; cerebrotective; hypotensive; tranquilizer; vulnerary; ophthalmological; cell proliferative disorder; actinic keratosis; anorectic; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; psoriasis; cancer; neurological disorder; stroke; Alzheimer's disease; Huntington's disease; Parkinson's disease; cardiovascular disorder; epilepsy; hypertension; varicose vein; vasculitis; dysphagia; dyspepsia; anorexia; gastrointestinal disorder; pancreatitis; autoimmune disorder; Addison's disease; Crohn's disease; acquired immune deficiency syndrome; AIDS; uveitis; infection; trauma; metabolic disorder; diabetes; obesity; osteoporosis; transgenic animal; gene therapy.

Homo sapiens.

Key Location/Qualifiers
 Domain 41..61 /label= Transmembrane_domain
 Domain 53..133 /label= 7_transmembrane_receptor_domain
 Domain 155..306 /label= 7_transmembrane_receptor_domain

WO200157085-A2.

09-AUG-2001.

01-FEB-2001; 2001WO-US03455.

02-FEB-2000; 2000US-0180093.

11-FEB-2000; 2000US-0182045.

(INCY-) INCYTE GENOMICS INC.

Baughn MR, Au Young J, Yue H,

WPI; 2001-488869/53.

N-PSDB; AAD12954.

Novel isolated human G-protein coupled receptor useful for diagnosing, preventing and treating cell proliferative, neurological, cardiovascular, gastrointestinal, autoimmune/inflammatory and metabolic disorders -

Claim 1; Page 119-120; 138pp; English.

The present sequence is human G-protein coupled receptor-11 (GCRC-11) protein. The present invention relates to GCRC protein and nucleic acids encoding them. GCRC protein, its agonist or antagonist are useful for treating diseases or conditions associated with decreased expression or overexpression of functional GCRC in a patient, where the disorder is selected from cell proliferative disorders such as actinic keratosis, arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, psoriasis, and cancer, neurological disorders such as epilepsy, stroke, Alzheimer's disease, Huntington's disease, Parkinson's disease, cardiovascular disorders such as hypertension, vasculitis, varicose veins, gastrointestinal disorders such as dysphagia, dyspepsia, anorexia, nausea, pancreatitis, autoimmune/inflammatory disorders such as acquired immunodeficiency syndrome (AIDS), Addison's disease, Crohn's disease, uveitis, viral, bacterial, fungal, parasitic, protozoal, helminthic infections, trauma and metabolic disorders such as diabetes, obesity, osteoporosis. GCRC proteins and their cDNAs are used to assess the effects of exogenous compounds on the expression of GCRC sequences. GCRC cDNA is useful to create knock in humanised animals (pigs) or transgenic animals (mice or rats) to model human disease, for therapeutic or diagnostic purposes, for somatic or germline gene therapy, to generate hybridisation probes useful in mapping the naturally occurring genomic sequence, and in molecular biological

XX techniques.
 XX
 XX Sequence 419 AA;
 Query March 100.0%; Score 2167; DB 22; Length 419;
 Best Local Similarity 100.0%; Pred. No. 2,60 191;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 C7 1 MWGSPFHLHFAAGYVPCGQWETIIIALVAYTVGVVWVNVNIIIVHRAAPDEIWA
 DB 14 MWGSPFHLHFAAGYVPCGQWETIIIPALLVAVGVVWVNVNIIIVHRAAPDEIWA
 C7 61 HSLILNLGLADLILPSADIPATAYSKVNDLQWPCVSSWPFHTQMAAKSLIVVVA 120
 DB 74 HSLILNLGLADLILPSADIPATAYSKVNDLQWPCVSSWPFHTQMAAKSLIVVVA 133
 C7 121 KVCFMVSPAPKOVSHNVTIKSVLVAIVTVASLLPLPEWFFSTPHDEEVMCLVTVPA 180
 DB 134 KVCFMVSPAPKOVSHNVTIKSVLVAIVTVASLLPLPEWFFSTPHDEEVMCLVTVPA 133
 C7 191 VAEENMEMEELLYLAPGLLEFFAGTIFWPAVTCYFFTHTEHFLIFSEVTVWEL 240
 DB 194 VAEENMEMEELLYLAPGLLEFFAGTIFWPAVTCYFFTHTEHFLIFSEVTVWEL 250
 C7 241 STAIISALLWLPENWVWVWHLKAAAGPAPPOGFIALSOVLWSESASSANPLIFVWSEEF 300
 DB 254 STAIISALLWLPENWVWVWHLKAAAGPAPPOGFIALSOVLWSESASSANPLIFVWSEEF 313
 C7 361 REGKGVWFWMMITFEPTVSESETEFAHSENLPTVPTTESPASIFEPVETSSGAP 320
 DB 314 REGKGVWFWMMITFEPTVSESETEFAHSENLPTVPTTESPASIFEPVETSSGAP 372
 C7 361 KTEKAEIPILPVEQFWHEPTVPSVQNNPIPWHEHICQTREDFV 406
 DB 374 KTEKAEIPILPVEQFWHEPTVPSVQNNPIPWHEHICQTREDFV 419
 RESULT 7
 AAG63344
 ID AAG63344 standard; Protein: 419 AA.
 AC
 AC AAG63344;
 DT 15-OCT-2001 (first entry)
 XX Amino acid sequence of a human G-protein coupled receptor protein.
 XX Human; G-protein coupled receptor, leukocyte, hypertension,
 KW autoimmune disease; heart failure; meningitis; atopic dermatitis;
 KW pneumonia; Alzheimer's disease; liver cirrhosis; Cickn's disease;
 KW diabetes; hepatitis; herpes; Hodgkin's disease; hypercholesterolemia;
 KW influenza; hepatitis; rheumatic fever; cancer; ulcer.
 XX Homo sapiens.
 CS
 EN WK2001:59106-A1.
 FN
 XX 16-AUG-2001.
 PD
 XX 07-FEB-2001; 2001WO-JF00851.
 XX
 XX 08-FEB-2000; 20000P-0035660.
 XX
 XX (TAKE) TAKEDA CHEM IND LTD.
 XX
 XX Miwa M, Shintani Y, Matsui H;
 XX
 XX WPI: 2001-4970/5/54.
 DR N-PSDB; AAH43029.
 XX
 XX New G protein coupled receptor: protein TGR2 and gene encoding it,
 PT useful for screening potential drugs for treating inflammatory,
 PT neurological and cardiovascular diseases .
 PT

XX
 XX
 XX The present sequence represents a human G protein coupled receptor
 CC protein. The protein is isolated from leukocytes. The protein is
 CC used in the treatment, prevention and diagnosis of a variety of
 CC diseases including hypertension, autoimmune diseases, heart failure,
 CC meningitis, atopic dermatitis, pneumonia, Alzheimer's disease, some
 CC arthritis, Crohn's disease, diabetic complications, atypical hemolytic
 CC Hodgkin's disease, hypercholesterolemia, influenza, hepatitis, cancer
 CC fever, cancer and ulcers.
 XX
 XX Sequence 419 AA;
 Query March 100.0%; Score 2167; DB 22; Length 419;
 Best Local Similarity 100.0%; Pred. No. 2,60 191;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 C7 1 MWGSPFHLHFAAGYVPCGQWETIIIALVAYTVGVVWVNVNIIIVHRAAPDEIWA
 DB 14 MWGSPFHLHFAAGYVPCGQWETIIIPALLVAVGVVWVNVNIIIVHRAAPDEIWA
 C7 61 HSLILNLGLADLILPSADIPATAYSKVNDLQWPCVSSWPFHTQMAAKSLIVVVA 120
 DB 74 HSLILNLGLADLILPSADIPATAYSKVNDLQWPCVSSWPFHTQMAAKSLIVVVA 133
 C7 121 KVCFMVSPAPKOVSHNVTIKSVLVAIVTVASLLPLPEWFFSTPHDEEVMCLVTVPA 180
 DB 134 KVCFMVSPAPKOVSHNVTIKSVLVAIVTVASLLPLPEWFFSTPHDEEVMCLVTVPA 133
 C7 191 VAEENMEMEELLYLAPGLLEFFAGTIFWPAVTCYFFTHTEHFLIFSEVTVWEL 240
 DB 194 VAEENMEMEELLYLAPGLLEFFAGTIFWPAVTCYFFTHTEHFLIFSEVTVWEL 250
 C7 241 STAIISALLWLPENWVWVWHLKAAAGPAPPOGFIALSOVLWSESASSANPLIFVWSEEF 300
 DB 254 STAIISALLWLPENWVWVWHLKAAAGPAPPOGFIALSOVLWSESASSANPLIFVWSEEF 313
 C7 361 REGKGVWFWMMITFEPTVSESETEFAHSENLPTVPTTESPASIFEPVETSSGAP 320
 DB 314 REGKGVWFWMMITFEPTVSESETEFAHSENLPTVPTTESPASIFEPVETSSGAP 372
 C7 361 KTEKAEIPILPVEQFWHEPTVPSVQNNPIPWHEHICQTREDFV 406
 DB 374 KTEKAEIPILPVEQFWHEPTVPSVQNNPIPWHEHICQTREDFV 419
 RESULT 8
 AAU04363
 ID AAU04363 standard; Protein: 419 AA.
 AC
 AC AAU04363;
 XX
 XX 23-OCT-2001 (first entry)
 DT
 XX Human G-protein coupled receptor, BRU9.
 DE
 XX Human; G-protein coupled receptor; (HCR), BRU9; atypical hemolytic
 KW lung cancer.
 KW
 XX Homo sapiens.
 OS
 XX WO200136471-A2.
 PN
 XX 25-MAY-2001.
 PD
 XX 16-NOV-2000; 2000WO-US31599.
 XX
 XX 17-NOV-1999; 99US-0166084.
 PR 17-NOV-1999; 99US-0166093.
 PR 17-NOV-1999; 99US-0166369.
 PR 23-DEC-1999; 99US-0171900.
 PR 23-DEC-1999; 99US-0171901.
 PR

PR 23-DEC-1999; 99US-0171902.
 PR 11-FEB-2000; 2000US-0181749.
 PR 14-MAR-2000; 2000US-0189258.
 PP 14-MAR-2000; 2000US-0189258.
 PP 10-APR-2000; 2000US-0195898.
 PR 10-APR-2000; 2000US-0195898.
 PR 10-APR-2000; 2000US-0196078.
 PP 28-APR-2000; 2000US-0200419.
 PR 12-MAY-2000; 2000US-0201630.
 PR 12-JUN-2000; 2000US-0210741.
 PR 12-JUN-2000; 2000US-0210982.
 PR 21-AUG-2000; 2000US-0226760.
 PR 26-SEP-2000; 2000US-0235418.
 PR 26-SEP-2000; 2000US-0235779.
 PR 20-OCT-2000; 2000US-0242332.
 PR 20-OCT-2000; 2000US-0242343.
 XX (APEN-) APENA PHARM INC
 PA Chen R, Dang HT, Lowitz KP;
 PI WPI; 2001-355616/37.
 DR N-PSDB; AAS07936.
 XX Endogenous and non-endogenous versions of human G-protein coupled
 PT receptors for direct identification of candidate compounds as agonists,
 PT inverse agonists or partial agonists for use as therapeutic agents -
 XX Claim 5; Page 91-92; 160pp; English.
 PS The sequence represents a human G-protein coupled receptor (GPCR),
 CC hRUP9. The endogenous and non-endogenous, constitutively activated
 CC versions of human G-protein coupled receptors (GPCR), are useful for
 CC direct identification of candidate compounds as receptor agonists,
 CC inverse agonists or partial agonists having applicability as therapeutic
 CC agents for treating diseases related to GPCR, e.g. lung cancer.
 CC Non-endogenous version of human GPCRs are also utilized in research
 CC settings and in vitro and in vivo system, incorporating GPCRs can be
 CC utilised to elucidate and understand the roles these receptors
 CC play in the human condition, both normal and diseased.
 XX Sequence 419 AA;
 SQ Query Match 100.0%; Score 2167; DB 22; Length 419;
 Best Local Similarity 100.0%; Pred. No. 2.6e-191;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0,
 QY 1 MNVSFAHLHPAGGYPSPDSQDWRITIPALLVAVCLVGVGNLCVIGILLHNAWKGPSMI 60
 DB 14 MNVSFAHLHPAGGYPSPDSQDWRITIPALLVAVCLVGVGNLCVIGILLHNAWKGPSMI 73
 QY 61 HSLILNLSLACLILLPSAPIRATAYSKSVWDLGWFCVCKSSDWFIHTCWAAKSLTIVVVA 120
 DB 74 HSLILNLSLACLILLPSAPIRATAYSKSVWDLGWFCVCKSSDWFIHTCWAAKSLTIVVVA 133
 QY 121 KVCFFMVASDEPAKQVSHNYITWSVLVAITWTVASLLPLPEWFFSTIRHIEGVEMCLVDVPA 190
 DB 134 KVCFFMVASDEPAKQVSHNYITWSVLVAITWTVASLLPLPEWFFSTIRHIEGVEMCLVDVPA 193
 QY 181 VAEEFMSMCKLYELLAFGLPLEFASFYFWRAYDOCKRGTKTQNLNRIQSKQVTVMLL 240
 DB 194 VAEEFMSMCKLYELLAFGLPLEFASFYFWRAYDOCKRGTKTQNLNRIQSKQVTVMLL 253
 QY 241 SIATISALLWLPBWAVLWVHLKAAGPAPPQGFIALSQVLMFSSISANPLIFLVMSEEF 300
 DB 254 SIATISALLWLPBWAVLWVHLKAAGPAPPQGFIALSQVLMFSSISANPLIFLVMSEEF 313
 QY 301 PEGLFKQVWMMITKPPVTVSSESTETPANSSEGIPOKVPFSESPASIPKEKESSPSSGKG 360
 DB 314 PEGLFKQVWMMITKPPVTVSSESTETPANSSEGIPOKVPFSESPASIPKEKESSPSSGKG 373
 QY 361 FTEVAETIPLPDPVQFHERDTPVSVQNDPPIPWEHEDQETGEGVK 406

Db 374 KTEKAEIPLPDPVQFHERDTPVSVQNDPPIPWEHEDQETGEGVK 419

RESULT 9

AAU01848
 ID AAU01848 standard; Protein; 419 AA.

XX AC AAU01848;

XX DT 07-SEP-2001 (first entry)

XX DE Human DNA G-protein coupled receptor, PFI-001.

XX KW Human; G-protein coupled receptor; PFI-001; mutant;

XX KW chromosome 5; antibody; immunogen; signal transduction;

XX KW obesity; diabetes; metabolic disease; neurodegeneration;

XX KW psychotherapeutics; urogenital disease; reproduction; sexual medicine;

XX KW inflammation; cancer; tissue repair; dermatology; skin pigmentation;

XX KW photoregulation; frailty; osteoporosis; cardiovascular disease;

XX KW gastrointestinal disease; anti-infection; allergy; respiratory disease;

XX KW sensory organ disorder; sleep disorder; hair loss; melanin.

XX OS Homo sapiens.

XX PN EP1090989-A1.

XX PD 11-APR-2001.

XX PF 06-OCT-2000; 2000EP-0308851.

XX PR 08-OCT-1999; 99GB-0023889.

XX PA (PFI-001) PFIZER LTD.

XX PA (PFI-001) PFIZER INC.

XX PI Harland L;

XX DR WPI; 2001-302045/32.

XX DR N-PSDB; AAS03392.

XX PT New human G-protein coupled receptor (GPCR) polynucleotide and

PT polypeptide, useful in drug screening, as well as diagnosing or

PT treating diseases associated with signal transduction, e.g. obesity,

PT inflammation, tissue repair or cancer -

XX Claim 22; Page 19; 46pp; English

XX The sequence represents PFI-001, a Human G-protein coupled receptor.

CC The gene encoding PFI-001 is located on human chromosome 5.

CC Antibodies against PFI-001 and compounds which modulate its

CC activity are useful as pharmaceuticals, for manufacturing a

CC medicament for treating a patient having a need to modulate (i.e.

CC (selectively) antagonise or agonise) PFI-001, and for evaluating and/or

CC screening agents that can modulate PFI-001. The nucleic acid is also

CC useful in gene therapy. The nucleic acid and encoded protein are useful

CC for screening drug candidates for treating diseases associated with

CC signal transduction such as obesity, diabetes and metabolic disease,

CC neurological disease, psychotherapeutics, urogenital disease,

CC reproduction and sexual medicine, inflammation, cancer, tissue repair,

CC dermatology, skin pigmentation, photoregulation, frailty, osteoporosis,

CC cardiovascular disease, gastrointestinal disease, anti-infection,

CC allergy and respiratory disease, sensory organ disorders, sleep disorders

CC or hair loss.

XX Sequence 419 AA;

SQ Query Match 100.0%; Score 2167; DB 22; Length 419;

Best Local Similarity 100.0%; Pred. No. 2.6e-191;

Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNVSFAHLHPAGGYPSPDSQDWRITIPALLVAVCLVGVGNLCVIGILLHNAWKGPSMI 60

DB 14 MNVSFAHLHPAGGYPSPDSQDWRITIPALLVAVCLVGVGNLCVIGILLHNAWKGPSMI 73

Best Local Similarity 99.8%; Pred No 4 8e-191;
Matches 405; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNVSFAHLHPAGGYLPSDSQDWRTIIPALLVAVCLVGFVGNLCVIGILLHNAAKGPMSI 60
DB 14 MNVSFAHLHPAGGYLPSDSQDWRTIIPALLVAVCLVGFVGNLCVIGILLHNAAKGPMSI 73

QY 61 HSLILNLSLADLSLLPSAPIRATAYSKSVMDLGFVCKSSDWFHTCMAAKSLTIIVVA 120
DB 74 HSLILNLSLADLSLLPSAPIRATAYSKSVMDLGFVCKSSDWFHTCMAAKSLTIIVVA 133

QY 121 KVCFMVASTPAKQVSHNYTISVLAIVTASLLPLPEWFFSTIRHHGVEMCLVDVPA 180
DB 134 KVCFMVASTPAKQVSHNYTISVLAIVTASLLPLPEWFFSTIRHHGVEMCLVDVPA 193

QY 181 VAEFPMSPKTYPLAFGLPLFPASFPWPAYDQCKKPTQNLKRGKRSQVTVMLL 240
DB 194 VAEFPMSPKTYPLAFGLPLFPASFPWPAYDQCKKPTQNLKRGKRSQVTVMLL 253

QY 241 STAIISALLMLPEWVAWLWWHLKAAGPAPPQGFIALSQVLMFSSANPLIFLVMSEEF 300
DB 254 STAIISALLMLPEWVAWLWWHLKAAGPAPPQGFIALSQVLMFSSANPLIFLVMSEEF 313

QY 301 REGKGVWVWMTYKPTVSESETPAGNSGELPDVPSPESPASTPEKEKPSPPSSGKG 360
DB 314 REGKGVWVWMTYKPTVSESETPAGNSGELPDVPSPESPASTPEKEKPSPPSSGKG 373

QY 361 KTEKAEIPLPDVEQFHWHERDTVPSVQDNDPIPWEHEDQETGEGVK 406
DB 374 KTEKAEIPLPDVEQFHWHERDTVPSVQDNDPIPWEHEDQETGEGVK 419

RESULT 14
AAG64120
ID AAG64120 standard; Protein; 419 AA.
XX AAG64120;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human G protein-coupled receptor GPRv16.
XX
KW Human; guanosine triphosphate binding protein-coupled receptor;
KW G protein-coupled receptor; GPRv8; GPRv12; GPRv16; GPRv21; GPRv40;
KW GPRv47; GPRv51; GPRv71; GPRv72; cancer; liver cirrhosis;
KW Alzheimer's disease; cytostatic; hepatotropic; neurotropic;
KW neuroprotective; gene therapy; peptide therapy.
XX
OS Homo sapiens.
XX
XX WO200148188-A1.
XX
XX 06-JUL-2001
XX
XX 28-DEC-2000; 2000WQ-JF00409.
XX
XX 28-DEC-1999; 00JP 0375152
PR 31-MAR-2000; 2000JP 010339.
XX
XX (HELI-) HELIX RFS INST.
XX
XX Matsumoto S, Oda T, Saito Y, Morikawa N, Yoshida K, Suwa M;
PI Sugiyama T, Kishimoto T, Kanzaki K, Yasuda S, Inoue Y;
XX WPI; 2001-425662/45.
DR N-PSDB; AAH73533.
XX
XX New DNA encoding guanosine triphosphate binding protein coupled
PT receptors and their expression products for screening potential
PT anticancer and neurotropic drugs and in diagnosis of these diseases
XX
XX Example 1; Page 108-111; 170pp; Japanese.
PS
XX

CC The invention relates to nine human guanosine triphosphate binding
CC protein (G protein)-coupled receptors designated GPRv8, GPRv12, GPRv16,
CC GPRv21, GPRv40, GPRv47, GPRv51, GPRv71 and GPRv72, and to the
CC genes encoding them. These genes and proteins and antibodies against
CC the protein are useful in the treatment, prevention, diagnosis and
CC investigation of diseases associated with G protein-coupled receptors,
CC including cancer, cirrhosis of the liver and Alzheimer's disease.
CC The present sequence is a G protein coupled receptor of the invention.

XX Sequence 419 AA;
SQ

Query Match 99.9%, Score 2164, DB 22; Length 419;
Best Local Similarity 99.8%; Pred. No. 4 8e-191;
Matches 405; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNVSFAHLHPAGGYLPSDSQDWRTIIPALLVAVCLVGFVGNLCVIGILLHNAAKGPMSI 60
DB 14 MNVSFAHLHPAGGYLPSDSQDWRTIIPALLVAVCLVGFVGNLCVIGILLHNAAKGPMSI 73

QY 61 HSLILNLSLADLSLLPSAPIRATAYSKSVMDLGFVCKSSDWFHTCMAAKSLTIIVVA 120
DB 74 HSLILNLSLADLSLLPSAPIRATAYSKSVMDLGFVCKSSDWFHTCMAAKSLTIIVVA 133

QY 121 KVCFMVASTPAKQVSHNYTISVLAIVTASLLPLPEWFFSTIRHHGVEMCLVDVPA 180
DB 134 KVCFMVASTPAKQVSHNYTISVLAIVTASLLPLPEWFFSTIRHHGVEMCLVDVPA 193

QY 181 VAEFPMSPKTYPLAFGLPLFPASFPWPAYDQCKKPTQNLKRGKRSQVTVMLL 240
DB 194 VAEFPMSPKTYPLAFGLPLFPASFPWPAYDQCKKPTQNLKRGKRSQVTVMLL 253

QY 241 STAIISALLMLPEWVAWLWWHLKAAGPAPPQGFIALSQVLMFSSANPLIFLVMSEEF 300
DB 254 STAIISALLMLPEWVAWLWWHLKAAGPAPPQGFIALSQVLMFSSANPLIFLVMSEEF 313

QY 301 REGKGVWVWMTYKPTVSESETPAGNSGELPDVPSPESPASTPEKEKPSPPSSGKG 360
DB 314 REGKGVWVWMTYKPTVSESETPAGNSGELPDVPSPESPASTPEKEKPSPPSSGKG 373

QY 361 KTEKAEIPLPDVEQFHWHERDTVPSVQDNDPIPWEHEDQETGEGVK 406
DB 374 KTEKAEIPLPDVEQFHWHERDTVPSVQDNDPIPWEHEDQETGEGVK 419

RESULT 15
AAU73244
ID AAU73244 standard; Protein; 418 AA.
XX AAU73244;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human potential G protein-coupled receptor.
XX
KW Human; G protein-coupled receptor; GPCR; GALT4, galanin receptor;
KW Alzheimer's disease; amyotrophic lateral sclerosis; asthma;
KW atherosclerosis; basal cell carcinoma; breast carcinoma; cardiovascular;
KW chondrosarcoma; chronic obstructive pulmonary disease; Crohn's disease;
KW depression; epilepsy; macular degeneration; lymphoma; melanoma;
KW multiple sclerosis; osteoarthritis; osteoporosis; Parkinson's disease;
KW psoriasis; rheumatoid arthritis; schizophrenia; ulcerative colitis;
KW tuberculosis; cognition disorder; memory disorder; anorexia;
KW hormonal release disorder; cardiovascular activity disorder;
KW pain perception disorder; obesity; diabetes; diabetes; obesity;
KW diabetes; hyperlipidaemia; stroke; gene therapy.
XX
OS Homo sapiens.
XX
XX WO200185791-A1.
PN
XX
PD 15-NOV-2001.
XX
XX 11-MAY-2001; 2001WO-US15332.
PF

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OM protein - protein search, using sw model

Run of: January 28, 2003, 11:48:36 ; Search time 35 Seconds

(without alignments)
2390.147 Million cell updates/sec

Title: US-09-828-432-3

Perfect score: 2167

Sequence: 1 MMSVFAHLRAGGVLPDSQC QMNPFWHEHEDQETGEVVK 406

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 21:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_todent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriaph:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2167	100.0	419	Q8TDV0	Q8tdv0 homo sapien
2	251	11.6	380	Q9NFV1	Q9nfv1 lymanaea sta
3	247.5	11.4	380	Q9NFV2	Q9nfv2 lymanaea sta
4	236	10.9	444	Q23497	Q23497 caenorhabdi
5	232.5	10.7	380	Q9NFV0	Q9nfv0 lymanaea sta
6	230.5	10.6	411	Q9W613	Q9w613 gallus gall
7	230	10.6	443	Q2514	Q2514 cavia porce
8	228	10.5	452	Q9JKN0	Q9jkn0 mus musculu
9	227	10.5	422	Q9VH27	Q9vh27 rattus norv
10	220.5	10.2	380	Q9NFV3	Q9nfv3 lymanaea sta
11	218	10.1	329	Q9VAU0	Q9va0 drosophila
12	218	10.1	357	Q9NBC8	Q9nbc8 drosophila
13	217.5	10.0	377	Q9QGM3	Q9qgm3 gallus gall
14	214.5	9.9	361	Q9WPA2	Q9wpa2 bombyx mori
15	214.5	9.8	385	Q9JKA0	Q9jka0 mus musculu
16	214.5	9.8	394	Q9UDE6	Q9ude6 homo sapien

17	208.5	9.6	375	6	Q97505	Q97505 sus scrofa
18	205.5	9.5	432	11	Q924C9	Q924c9 rattus norv
19	205	9.5	436	11	Q8VCC7	Q8vcc7 mus musculu
20	205	9.5	463	11	Q9EPJ7	Q9epj7 mus musculu
21	203	9.4	394	5	Q9U721	Q9u721 drosophila
22	202.5	9.3	346	6	Q95K56	Q95k56 ovis aries
23	202.5	9.3	391	5	Q44149	Q44149 caenorhabdi
24	201.5	9.3	379	5	Q9T760	Q9t760 branchiosteo
25	199	9.2	436	11	Q9DBV6	Q9dbv6 mus musculu
26	198	9.1	451	5	Q9VWQ1	Q9vwq1 drosophila
27	197.5	9.1	354	13	Q97499	Q97499 xenopus lae
28	195.5	9.0	346	11	Q91Y73	Q91y73 mus musculu
29	195	9.0	370	13	Q9UML5	Q9uml5 fugu rubrip
30	195	9.0	517	5	Q8T0S8	Q8t0s8 drosophila
31	194.5	9.0	346	4	Q96GE0	Q96ge0 homo sapien
32	194.5	9.0	356	4	Q96TF2	Q96tf2 homo sapien
33	193.5	8.9	404	13	Q9DFB0	Q9dfb0 catostomus
34	193.5	8.9	405	11	Q924N0	Q924n0 mus musculu
35	193.5	8.9	521	5	Q9VAD2	Q9vad2 drosophila
36	193	8.9	311	11	Q9T1P6	Q9t1p6 cavia porce
37	193	8.9	340	6	Q8S054	Q8s054 macaca fasc
38	192	8.9	340	4	Q969V1	Q969v1 homo sapien
39	191.5	8.8	380	13	Q9DGG6	Q9dgg6 carassius a
40	189.5	8.7	315	6	Q9GKP7	Q9gkp7 sus scrofa
41	189.5	8.7	367	13	Q9PVP9	Q9pvp9 carassius a
42	189	8.7	340	4	Q9EXA8	Q9exa8 homo sapien
43	189	8.7	430	4	Q9ERN3	Q9ern3 homo sapien
44	188.5	8.7	367	13	Q9FVG0	Q9fvq0 carassius a
45	188.5	8.7	410	5	Q9V857	Q9v857 drosophila

ALIGNMENTS

RESULT 1

ID	Q8TDV0	PRELIMINARY;	PRT;	419 AA.
AC	Q8TDV0;			
DT	01-JUN-2002 (TrEMBLrel. 21, Created)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)			
DE	Putative G-protein coupled receptor.			
GN	GPCR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
PP	SEQUENCE FROM N.A.			
RA	Takeda S., Kadawala S., Haga T., Takasuo H., Miraku S.,			
RT	Identification of G protein-coupled receptor genes from the human			
RT	genome sequence."			
RL	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB083592; BAB89305.1; -			
KW	Receptor.			
SQ	SEQUENCE 419 AA; 46637 MW; 76978068B1PC6140 CPC64;			

Query Match 100.0%; Score 2167; DB 4; Length 419;
Best Local Similarity 100.0%; Pred. No. 8.2e-165;

Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MMSVFAHLRAGGVLPDSQCQWETIIIPALLVAVCLVCFVGNLCVIGILLINAWGPTSMI	60
Db	14	MMSVFAHLRAGGVLPDSQCQWETIIIPALLVAVCLVCFVGNLCVIGILLINAWGPTSMI	73
Qy	61	HSLIINSLADLSLLLSAPITATVATVSKVNDLQWPFVCKSSDWFIHTCMAKSLTIWVA	120
Db	74	HSLIINSLADLSLLLSAPITATVATVSKVNDLQWPFVCKSSDWFIHTCMAKSLTIWVA	133
Qy	121	KVCFWYASDPKQVSYIHNYITWSVLVAITWVASLLPLPEWFFSTIPHHGVEMCLVWVA	180
Db	134	KVCFWYASDPKQVSYIHNYITWSVLVAITWVASLLPLPEWFFSTIPHHGVEMCLVWVA	193

QY 181 VAEPEEEMCKLYPI LAFGLPEFASFWPAVDCKKKCKTKTONLPNOIRSKQVTVMLL 240
 Db 194 VAEPEEEMCKLYPI LAFGLPEFASFWPAVDCKKKCKTKTONLPNOIRSKQVTVMLL 253
 QY 241 SIAIISALLLWLPWVAWLWHLKAAGPAPQGFIALSOVLMSISSANPLIFLWSEEF 300
 Db 254 SIAIISALLLWLPWVAWLWHLKAAGPAPQGFIALSOVLMSISSANPLIFLWSEEF 313
 QY 301 PEGLKFWWMMITPKPTVSQETPAGNSGELPDVVPSPSPASIPPEYSSSSSGHG 360
 Db 314 PEGLKFWWMMITPKPTVSQETPAGNSGELPDVVPSPSPASIPPEYSSSSSGHG 373
 QY 361 PTEFAPIPIIPVEQFWHEPDTVFSQNDPDPWEHEPDTREGV 406
 Db 374 PTEFAPIPIIPVEQFWHEPDTVFSQNDPDPWEHEPDTREGV 419

RESULT 2

Q9NEV1 PRELIMINARY; PRT; 380 AA.
 AC Q9NEV1;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE G-protein coupled receptor
 GN ORPH 3.
 OS Lymnaea stagnalis (Great pond snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
 OC Lymnaeidae; Lymnaea.
 OX NCBI_TaxID=6523;
 RN [1]
 RP SEQUENCE FROM N A.
 RA Saunders S.F., Burke J.F., Benjamin P.R.;
 PT "Multimeric G-protein binding sites in the promoter regions of a family of
 FT alpha 5 protein-coupled receptors related to the vertebrate galanin
 RT and nociceptin/orphanin-FQ receptor families";
 RL Submitted (Oct-1999) to the EMBL/GenBank/DBS databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AJ270461; CAFE7264.1;
 DR HSSP: P02660; IPR4
 IF IPR000013; IPR000076; GPCR_FH_nbsp
 DR Pfam: PF00001; 7tm1.1;
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PR01570; NPPEPCEPTOR.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1;
 DR PROSITE: PS0262; G-PROTEIN_RECEP_FL_2;
 FW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane
 CQ SEQUENCE: see AA, 436-444 MW, 47246 Da; pI=5.4; CD=1; GPCR64;

Query Match 11.6%; Score 251; DB 5; Length 380;
 Best Local Similarity 23.2%; Pred. No. 4.2e 13;
 Matches 89; Conservative 68; Mismatches 153; Indels 74; Gaps 13.

QY 11 AGGY-----LPDS-----QDW-----RTIIPALLVAVCLVGV 39
 Db 3 AGLADAHILNLSGSGVSTIYPTNTAAAHNESNMGTVEYVLIIVTPISGICGLG 62
 QY 40 GNLGVGILLHNWAKGPPSMHSLNLSLADLSLLESAPATAYSKVMGLGWCKY 99
 Db 63 GNSLIVVAVSD--KIMPNTNTNIIIPAVADULFLPCVPTATYALPVWPFSDIGCK 120
 QY 100 GSEWFTHIINAAKELTIIVVAVKVFVYASPPAKGVCIHR-VTIWVSLVAITVA-----SL 154
 Db 121 MTQYAMVVCAYAVYTLVMSLDYLVAVVHAIPSMILPSEBNTWPAIILWIIICGNT 180
 QY 155 IPIPEPFSTIRHHEGVNML-----VDVAVABEENS---MCKLYPL-----LAFGLPE 203
 Db 161 ILQGVFNVTWVHSGNPSATLNLKELFEKAEAGFAFFSELFEGYVILGVITMLMYGLM 240
 QY 204 PASEYLPWPAVQCKPKTHKTPNLNLPNIPSPQVTVMILLSIATLSALLWLPEWVAWLWVHL 263
 Db 241 PILYGV-----VPTGQNSRESIPAKYPPVTPMVIVVVISAIQWLIQIILFAEP 292

QY 264 KAAGPAPQGFIALSOVLMSISSANPLIFLWSEEFEGHKGW 300
 Db 293 HAPHTIFHISTMEAFANCLAYMGCVPILYAFLENEFFEFELSTETVEFWYFVW 331
 QY 312 ----ITKKPTVSPSQETPAGNSE 331
 Db 353 VPPTVTEK-PTTTTTKQTGVNSK 376

RESULT 3

Q9NEV2 PRELIMINARY; PRT; 380 AA.
 AC Q9NEV2;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE G-protein coupled receptor
 GN ORPH 2.
 OS Lymnaea stagnalis (Great pond snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
 OC Lymnaeidae; Lymnaea.
 OX NCBI_TaxID=6523;
 RN [1]
 RP SEQUENCE FROM N A.
 RA Saunders S.F., Burke J.F., Benjamin P.R.;
 PT "Multimeric G-protein binding sites in the promoter regions of a family of
 FT alpha 5 protein-coupled receptors related to the vertebrate galanin
 RT and nociceptin/orphanin-FQ receptor families";
 RL Submitted (Oct-1999) to the EMBL/GenBank/DBS databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AJ270460; CAFE7263.1;
 DR HSSP: P02660; IPR4
 IF IPR000013; IPR000076; GPCR_FH_nbsp
 DR Pfam: PF00001; 7tm1.1;
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PR01570; NPPEPCEPTOR.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1;
 DR PROSITE: PS0262; G-PROTEIN_RECEP_FL_2;
 FW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane
 CQ SEQUENCE: see AA, 436-444 MW, 47246 Da; pI=5.4; CD=1; GPCR64;

Query Match

11.4%; Score 247.5; DB 5; Length 380;
 Best Local Similarity 22.7%; Pred. No. 7.9e 12;
 Matches 79; Conservative 68; Mismatches 144; Indels 69; Gaps 13.

QY 23 FTIIPALLVAVCLVGVNLSGSGVSTIYPTNTAAAHNESNMGTVEYVLIIVTPISGICGLG 39
 Db 46 PIIVPTIPGVICTLGLSGSLIVPVVSD--KIMPNTNTNIIISLAVAKELFLVPTET 104
 QY 83 ATAYSKSWLWLEFVYKSSSWFTHIWAAPKHLIVVAVKVFVYASPPAKGVCIHR-VTI 143
 Db 104 ATGVALPVWPFSDIGCK-PTIIVAVVAVYAVAVYTVIVMSIEFTAVVHSDVMTSEBNT 164
 QY 142 WSVVAVATVA--SILSIFFEFEFTIRHHEGVNML-----VDVAVABEENS---MCKLYPL 199
 Db 164 WFAILLWIIICGNTPIILGCGVFNVHSGNPSATLNLKELFEKAEAGFAFFSELFEGYVILG 240
 QY 191 KLYPL-----LAFGLPEFAYFWAYCQYFF 203
 Db 224 YVILPVGLVITMLMYGLM-----KPILYGVWVFNVTWVHSGNPSATLNLKELFEKAEAGFAFF 240
 QY 240 LSTATISALLWLPEWVAWLWVHAIPSMILPSEBNTWPAIILWIIICGNT 180
 Db 269 VIVVVISAIQWLIQIILFAEPFGHAPNTIPHISTMEAFANCLAYMGCVPILYAFLENEFF 300
 QY 300 PEGLKFWW-----FWTAKPTVSPSQETPAGNSE 331
 Db 329 PPSPPFLQCTESSERMEVETNPVETVTP-PTTFPGGVNSK 376

RESULT 4


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CC 1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
DR EMBL; AF131057; AAF31017.1;
DR HSP; P29274; IMH.
DR InterPro; IPR000276; GPCR_Phosph.
DR Pfam; PF00001; 7tm 1; 1
DR PRINTS; PS00237; GPCRPHOSPN.
DR PRINTS; PR01565; NEUROMEDINUR.
DR PRINTS; PR01570; NPFRRECEPT.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_2; 1.
DR G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 411 AA; 47090 MW; 4584160A44150 CP064;

Query Match
Best Local Similarity 24.1%; Pred No 26-10;
Matches 90; Conservative 50; Mismatches 142; Indels 57; Gaps 12.

CY 22 WPTIIFALLVA-VLVGVFVSNVIGIILHNAPFSPSHLSLNLADLSLLFSAP 80
DB 34 QVALNAVAATLIVVSVVATVVMVAIL--AHFPMPTVTNYFVLAATAFASMSAFRTV 91
CY 81 IPATAYSKSWLGMVFCVSSSWFHTTMAAVALSITVVVAVVCFVYASDPQVSHNYT 140
DB 92 VNFYVTHNEWYSGILYCRPHNFFPIAAVFASTVSMATAIDPYMAITHPI--QPRISATA 150
CY 141 TMSVLVAINTVASLLPLPEWFFSTIRHHEGVEMCLVDVDAVAEERMSFGKLY----- 193
DB 151 TKVIVVIMLIALFAFPQYQYVATELPLPLVLUWMP---EHSVVGVKTYHGMVIL 207
CY 194 ... PLALFTLFFFAFYFWAYCVPYPTVYTHLPTSPYQVVMGLSTALIS-AL 248
DB 208 IYELDLVLGVAVTVSVITLWAS---EIPGDSNDPYHPLVSAKPKVVMVIMLVCTPAL 263
CY 249 LNL .....PEWAVLWHLKAAAGAPFPQFIALGVLMFSISSANFLPLVM 296
DB 264 QWLVNYVYETLVYFHWLQFPI .....QWVLAVMWLAWSSTMTKPIIVYGL 312
CY 297 SEFEFEGIKVWPMWMTKPPPTVSSQETPAENSEGLPPV 336
DB 313 NDFPVGVKHAFFWC-----PFVS-----AAVEGLEMK 341

RESULT 7
Q92494
ID Q92494 PRELIMINARY, PST, 443 AA
AC Q92494
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Neurokinin B receptor
GN NK3.
OS Cavia porcellus (Guinea pig)
OC Eukaryota, Metazoa, Chordata; Craniata, Vertebrata, Euteleostomi,
OC Mammalia, Eutheria, Rodentia, Myiologthi, Caviidae, Cavia.
CX NIH_TaxID=10341,
RN [1]
RN SEQUENCE FROM N.A.
RA Stumm R.K., Schaefer M.K.H., Weihe E.;
RA "Cloning and sequencing of Guinea pig NK3 receptor",
PT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF255393; AAK49193.1;
DR InterPro; IPR000276; GPCR_Phosph.
DR Pfam; PF00001; 7tm 1; 1.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; NK3OWN_1
DR PROSITE; PS00262; G-PROTEIN_RECEP_FL_2; 1.
KW Receptor
SQ SEQUENCE 440 AA; 49516 MW; FR48BQAF505454D0 CP064;

Query Match
Best Local Similarity 10.6%; Score 230; DB 11; Length 440;
Matches 77; Conservative 61; Mismatches 129; Indels 46; Gaps 11;

CY 22 WPTIIFALLVAVLVGVFVSNVIGIILHNAPFSPSHLSLNLADLSLLFSAP 80

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DB 58 WEVALWSLAVAVAVAVLGNLVIMVL--AHFPMPTVTNVSQVAVLAAAMALNAL 119
CY 81 IPATAYSKSWLGMVFCVSSSWFHTTMAAVALSITVVVAVVCFVYASDPQVSHNYT 140
DB 92 VNFYVTHNEWYSGILYCRPHNFFPIAAVFASTVSMATAIDPYMAITHPI--QPRISATA 150
CY 141 TMSVLVAINTVASLLPLPEWFFSTIRHHEGVEMCLVDVDAVAEERMSFGKLY----- 193
DB 151 TKVIVVIMLIALFAFPQYQYVATELPLPLVLUWMP---EHSVVGVKTYHGMVIL 207
CY 194 ... PLALFTLFFFAFYFWAYCVPYPTVYTHLPTSPYQVVMGLSTALIS-AL 248
DB 208 IYELDLVLGVAVTVSVITLWAS---EIPGDSNDPYHPLVSAKPKVVMVIMLVCTPAL 263
CY 249 LNL .....PEWAVLWHLKAAAGAPFPQFIALGVLMFSISSANFLPLVM 296
DB 264 QWLVNYVYETLVYFHWLQFPI .....QWVLAVMWLAWSSTMTKPIIVYGL 312
CY 297 SEFEFEGIKVWPMWMTKPPPTVSSQETPAENSEGLPPV 336
DB 313 NDFPVGVKHAFFWC-----PFVS-----AAVEGLEMK 341

RESULT 8
Q9JKNO
ID Q9JKNO PRELIMINARY, PST, 452 AA
AC Q9JKNO
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Neurokinin-3 receptor
GN TACR3.
OS Mus musculus (Mouse)
OC Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia, Eutheria, Rodentia, Sciuroidea, Muridae, Mus.
CX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RA Feild J.A., Brun K.A.;
RA "Molecular cloning and characterization of the murine neurokinin-3
RT receptor",
PT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DE SUBSTITUTION INFORMATION: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF233341; AAF62517.1;
DR HSP; F02699; IP88.
DR MOP; MGI_843648; Tacr3.
DR InterPro; IPR000276; GPCR_Phosph.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PS00237; GPCRPHOSPN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_FL_2; 1.
FW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 452 AA; 51026 MW; 7A46D400AD7FC444 CP064;

Query Match
Best Local Similarity 10.5%; Score 228; DB 11; Length 452;
Matches 90; Conservative 63; Mismatches 161; Indels 49; Gaps 10;

CY 22 WPTIIFALLVAVLVGVFVSNVIGIILHNAPFSPSHLSLNLADLSLLFSAP 80
DB 70 WPTALWSLAVLVVAVAVFVNIVIMIL--AHFPMPTVTNVSQVAVLAAAMALNAL 119
CY 81 IPATAYSKSWLGMVFCVSSSWFHTTMAAVALSITVVVAVVCFVYASDPQVSHNYT 140
DB 92 VNFYVTHNEWYSGILYCRPHNFFPIAAVFASTVSMATAIDPYMAITHPI--QPRISATA 150
CY 141 TMSVLVAINTVASLLPLPEWFFSTIRHHEGVEMCLVDVDAVAEERMSFGKLY----- 193
DB 151 TKVIVVIMLIALFAFPQYQYVATELPLPLVLUWMP---EHSVVGVKTYHGMVIL 207
CY 194 ... PLALFTLFFFAFYFWAYCVPYPTVYTHLPTSPYQVVMGLSTALIS-AL 248
DB 208 IYELDLVLGVAVTVSVITLWAS---EIPGDSNDPYHPLVSAKPKVVMVIMLVCTPAL 263
CY 249 LNL .....PEWAVLWHLKAAAGAPFPQFIALGVLMFSISSANFLPLVM 296
DB 264 QWLVNYVYETLVYFHWLQFPI .....QWVLAVMWLAWSSTMTKPIIVYGL 312
CY 297 SEFEFEGIKVWPMWMTKPPPTVSSQETPAENSEGLPPV 336
DB 313 NDFPVGVKHAFFWC-----PFVS-----AAVEGLEMK 341

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Db 196 FTTNDFLGPPTVQVTFRISSVYLPLMIISGLYMPIMPLWPGTGVPMKESQSGPKRVT 255
 QY 237 VMLLSIAISALLMLPEWAMLVWHLKAAGPAPPGGIAL-----SOVLMFSISSANPL 291
 Db 256 PLWVWVWAFASLWLPVGLILL-----LKSLSVETNTLTHVIVQVTAQTLAYSSSCINPL 311
 QY 292 IFLVWSEEFRE 302
 Db 312 LYAFLESEFRK 322

RESULT 13
 Q8QGM3 PRELIMINARY; PPT; 377 AA.
 ID Q8QGM3
 AC Q8QGM3 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DE Neurotrophin Y Receptor 4
 OS Gallus Gallus (Chicken)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus
 CX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lundell I., Boswell T., Larhammar D.;
 RT "Chicken Neurotrophin Y Family Receptor Y4: a Receptor with Equal
 RT Affinity for Pancreatic Polypeptide, Neuropeptide Y, and Peptide YY";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DP FMR.; AF410963; AAL84161 1;
 KW Receptor.
 SQ SEQUENCE 377 AA, 42372 MW, 92656.000PPTDIFDE CRC64,

Query Match 10.0%; Score 217.5; DB 13; Length 377;
 Best Local Similarity 22.8%; Pred. No. 1.9e-09;
 Matches 68; Conservative 66; Mismatches 125; Indels 39; Gaps 8;

QY 15 LVTFTVNLGVIGILLHNAWFKFSMHSLNLSLALSLLSLPSAPIATVSKVMSLG 94
 Db 52 VLGVGNLGLIAVAPQ KPTNTVNLISNLISLFLMLVCLPPTVVTWQYWIFG 109
 QY 95 WPTKSSWFIHTMAAKELITVVAFAVVFEMVAFKQVSHHNTVMSLVA----- 147
 Db 110 FVWCFTSFTQCTSVTSLSLVIAL... EPHQIINPTGAPPSTQAVLGIG 160
 QY 148 LWTVASLPLTFEMFESTIPHHESVE-----MLLVFPAVAEFSMSPKLY 193
 Db 161 VMTIATLNSLP-FLTTSLSLNLVYELLSHIMNFSYKVAIDNSWP--SEQHPLIYTTTL 217
 QY 194 PLLAFGLPLFFASFYFWPAYDCKYFG--TKTQNLRLNCPISKQVTVMLLSIAISALLW 250
 Db 218 LLLQVCIPLFIILCYLPIYLPIQPRFMFEKSEYENPAVCLPRINILLASWVAAPVW 277
 QY 251 LPWVWAMLV-WHLKAAGPAPPGGIALSOVLMFSISSANPLIFLWSEEFREGLKV 307
 Db 278 LPLPHVNTIVDWNKYIISPCHHNLIFSLCHLVAMASTCTVNPVIYGLNFKKVEKSL 335

RESULT 14
 Q8WPA2 PRELIMINARY; PPT; 361 AA
 ID Q8WPA2
 AC Q8WPA2
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DE Allatostatin Receptor RAP
 OS Bombyx mori (Silk moth)
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Bombycoidea; Bombycidae; Bombyx.
 CX NCBI_TaxID=7031;
 RN [1]

PP SEQUENCE FROM N.A.
 RC STRAIN=LYON 203 BA/LYON 300 AB;
 RX MEDLINE=21601656; PubMed=11590150;
 PA Secher T., Lenz G., Cazzamali G., Sorensen G., Williamson M.,
 PA Hansen G.N., Svane P., Grimelikhuitzen C.J.P.;
 RT "Molecular Cloning of a Functional Allatostatin Gut/Brain Receptor and
 RT an Allatostatin Receptor from the silkworm Bombyx mori";
 PI J. Biol. Chem. 276:47052-47060(2001)
 DR EMBL; AF303370; AAL47056.1; JOINED.
 DR EMBL; AF303368; AAL47056.1; JOINED.
 DR EMBL; AF303369; AAL47056.1; JOINED.
 DP FMR.; AP254742; AAG444631 1;
 DP InterPro; IPR002106; AA-RNA ligaseII.
 DP InterPro; IPR000276; GPCR_Phosphn.
 DP Pfam; PF00001; 7tm1.1;
 DR PRINTS; PR00237; GPCRHHODOPS.
 DR POSITIVE; PS00330; AA_TRNA_LIGASE_F_2; UNKNOW 1.
 DE POSITIVE; PS00337; G_PROTEIN_RECEP_F1_1; UNKNOW 1.
 DR POSITIVE; PS00342; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 361 AA, 40478 MW, 630282846PC3010A CRC64;

Query Match 9.9%; Score 214.5; DB 5; Length 361;
 Best Local Similarity 24.6%; Pred. No. 2e-09;
 Matches 84; Conservative 52; Mismatches 141; Indels 65; Gaps 12;

QY 25 IIPALLVAVCLGVGNLGVIGILLHNAWFKFSMHSLNLSLALSLLSLPSAPIAT 94
 Db 44 VSPDFGFIGVGLGNALVVLVAAN FGMSTTNLLIINLAVALLVFCVPTFT 101
 QY 85 AYSFSVWMLTWPFVSSDFHTTMAAKSLITVVAFAVVFEMVAFKQVSHHNTVMS 144
 Db 102 EYWPEWPFETWVYVGVFIVVAIASVILVLSLSEFMATVHIAKMEIF TEZIA 159
 QY 145 LVA---LWTVASLLPLP-----EWFTSTPHHSEVEMCLVDFPAVAEFSMSEKLY 193
 Db 160 LLATATVWVILTTATPVGICHGESEYSEYFNHSSCV-----FLEER--Y 204
 QY 194 PLLAPGLPLFFASE-----YEWPAVQCFPFTGTQNLNCPISKQVTVMLL 240
 Db 205 SKLQFMSFLSYVTPIALISVLYWCMTPWFSAPGVAPSPSP--PVTEMV 261
 QY 241 SLALISALLGLFEWAMLVWHLKAAGPAPPGGIAL LSVLMFSISSANPLIFLW 296
 Db 262 VVVWFAVWVPTIILL VKALNPHYITVFTVTAQVCHLVAMASTCTVNPVIYGLN 317
 QY 297 SEEFREGLKVWFKMITYE-----FVWSESETPATNS 330
 Db 318 SENPPVAPP---FVWYCPPPYNDGFSRPLCATFTPTTNNNS 356

RESULT 15
 Q8JF40 PRELIMINARY; PPT; 385 AA
 ID Q8JF40
 AC Q8JF40
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Somatostatin subtype 5 receptor.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathii; Murinae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 PP SEQUENCE FROM N.A.
 SC STRAIN=129/SV;
 PA O'Carroll A.-M.;
 RT "Cloning, sequence and tissue distribution of the gene encoding a
 RT mouse somatostatin subtype 5 receptor";
 PL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SURCELLULAR LOCATION INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY BELONGS TO FAMILY 1 OF 5-RELATED COUPLED RECEPTORS.
 DR EMBL; AF268067; AAF72547.1; --

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OM protein - protein search, using sw model

Run on: January 28, 2003, 11:44:21, Search time 21 Seconds
(without alignments)
1858.599 Million cell updates/sec

Title: US-09-828-432-3

Perfect score: 2167
Sequence: 1 MNVSFAHHPAGGYLPSDSQ.....QNDPIPWHEHDEQETGEGVK 406

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 293224 seqs, 36134422 residues

Total number of hits satisfying chosen parameters. 293224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	265	12.2	387	JC5949	galanin receptor 2
2	262.5	12.1	349	I59336	galanin receptor 1
3	236.5	10.9	423	B40470	glucocorticoid-ind
4	236	10.9	444	T27866	hypothetical prote
5	231	10.7	407	S23510	neurokinin 1 recep
6	229	10.6	419	A46226	somatostatin recep
7	227	10.5	407	A34357	neurokinin 1 recep
8	227	10.5	407	S20304	neurokinin 1 recep
9	224.5	10.4	410	A44081	kappa-type opioid
10	224	10.3	465	JQ1517	neurokinin 3 recep
11	223.5	10.3	443	D40470	glucocorticoid-ind
12	221	10.2	395	S55524	neurokinin 3 recep
13	221	10.2	407	JQ1274	neurokinin 1 recep
14	221	10.2	452	A34916	neurokinin 3 recep
15	218	10.1	357	JC7319	probable allatosta
16	217	10.0	363	I48261	angiotensin II rec
17	216.5	10.0	390	JH0374	tombasin receptor,
18	216.5	10.0	402	I56595	neurokinin 2 recep
19	215.5	9.9	384	S00516	neurokinin 2 recep
20	215.5	9.9	390	A36737	neurokinin 2 recep
21	214	9.9	363	JC2543	angiotensin II rec
22	214	9.9	384	S20303	neurokinin 2 recep
23	211.5	9.8	375	I39182	neuropeptide Y/pep
24	211	9.7	363	A44922	angiotensin II rec
25	210.5	9.7	368	JQ1059	neurokinin 2 recep
26	209.5	9.6	375	G02300	pancreatic polypep
27	208.5	9.6	444	A42685	cholecystokinin re
28	208.5	9.6	428	S30508	probable G protein
29	206.5	9.5	431	C40470	glucocorticoid ind

ALIGNMENTS

RESULT 1

JC5949

galanin receptor 2 - human

C:Species: Homo sapiens (man)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul 2003

C:Accession: JC5949

R:Bloomquist, B.T.; Beauchamp, M.R.; Zhelnin, L.; Brown, S.E.; Gore-Millse, A.R.; Gregor,

Biochem. Biophys. Res. Commun. 243, 474-479, 1998

A:Title: Cloning and expression of the human galanin receptor GalR2.

A:Reference number: JC5949; MUID:98153789; PMID:9480833

A:Accession: JC5949

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-387 <BL0>

A:Cross-references: GB:AF040630; NID:30321759; PIR:AC39634.1; PID:92921760

C:Superfamily: vertebrate rhodopsin

Query Match 12.2% Score 265; DB 2; Length 387;
Best Local Similarity 26.7%; Pred No 1 3e-13;
Matches 85; Conservative 53; Mismatches 154; Indels 26; Gaps 9;

Qy	12	GYLDEDCCTFTTIPALLVAVCLVGVHLCVIGILLHNWGFQPMVHSIINISLAD 71
Db	19	GGWRPE-----AVIVPLLFALIFVGVNTLVLAVALRGQ--QAVSTTLFLNLGVAD 71
Qy	72	LSLLIFSAFIPATAYSKSVWELGWFCVSSWFHTTMAAFSLTIIVVAVKVCWVASDPA 131
Db	72	LCFILLCCVFPQNTIYLDGWVFGSLCKAVHFLFLTMHASSFTLAAVSLDRYLAAYPL 131
Qy	132	KQVSHNVTIWSVLA---IWTVASLLPLPEWFFSTIPHHH--GVEMCIIVVPAVAFEEM 186
Db	132	HAFELP--TTHALAAAGLLIWLGLLFSST YLSVYVGSJLANLYTHTANSAFFPEAM 187
Qy	187	S-----MFGFLIFLAFGLPLFPASFYFWAYDQCFKFGTKTONLPNIPSKQVWMLSS 242
Db	188	DICTVFVSYLLFVLVGLTYTATLFIPLFAVTPV-AAGSGAPPAP- SVTRNLIV 241
Qy	243	AIISALLWLPWVWVWLWHLKAGPAPQGFIALSQVLMFSSISANPLFLVMSSEFRE 302
Db	242	AALFLCLWVHFHALLICVWFGQFPLTPATYALFILSHINSVANSCTNFIYVAVVCTPFR 301
Qy	303	GLKGVWVWMTTFPPTVS 320
Db	302	GPTTCAGLIGPAPGRS 319

RESULT 2

I59336

galanin receptor 1 - human

C:Species: Homo sapiens (man)

C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jul 2003

C:Accession: I59336; JC5901; G01765; G02528


```
Db 372 GPK-ATPSSLDLTSGSRNSRNSKVTIPESS 399

RESULT 6
A46226
somatostatin receptor 3 - human
C:Species: Homo sapiens (man)
C>Date: 21-Sep-1993 #sequence_revision 18 Nov 1994 #text_change 24 Nov 1999
C:Accession: A46226; S32501
P:Yanada, Y.; Reisine, T.; Law, S.F.; Ihara, Y.; Kubota, A.; Kagimoto, S.; Seino, M.; Sei
Mol. Endocrinol. 6, 2136-2142, 1992
A:Title: Somatostatin receptors, an expanding gene family: cloning and functional charact
A:Reference number: A46226, MUID:93149123, PMID:1337145
A:Accession: A46226
A:Molecule type: DNA
A:Residues: 1-418 <YAM>
A:Cross-references: Gb:M96738; NID:93384378, FID:AAA62522.1, PID:9338499
A>Note: sequence extracted from NCBI backbone (NCBIN:123685, NCBIPI:213690)
R:Corneiss, J.D.; Demchishyn, L.L.; Seeman, P.; van Tol, H.H.M.; Strikant, C.P.; Kent, G.;
FEBS Lett. 321, 279-284, 1993
A:Title: A human somatostatin receptor (SSTR3), located on chromosome 22, displays prefer
A:Reference number: S32501; MUID:93238970; PMID:8097479
A:Accession: S32501
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-418 <COR>
C:Genetics:
A:Gene: GDB:SSTR3
A:Cross-references: GDB:134187; OMIM:182453
A:Map position: 22q13.1-22q13.1
A:Introns: #status absent
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protei
F:81-106/Domain: transmembrane #status predicted <TM1>
F:118-139/Domain: transmembrane #status predicted <TM2>
F:159-181/Domain: transmembrane #status predicted <TM3>
F:203-233/Domain: transmembrane #status predicted <TM4>
F:255-282/Domain: transmembrane #status predicted <TM5>
F:289-316/Domain: transmembrane #status predicted <TM6>
F:17-30/Binding site: carbohydrate (Asn) (covalent) #status predicted <TM7>
F:116-191/Disulfide bonds: #status predicted
F:121-251-317, 312/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status
F:231/Binding site: phosphate (Thr) (covalent) (by CAMP-dependent kinase) #status predict
F:256/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F:412/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 10.6%, Score 229; DB 2; Length 418;
Best Local Similarity 23.4%, Pred. No. 1; 1e-10;
Matches 83; Conservative 63; Mismatches 160; Indels 48; Gaps 11;

QY 25 LIPALLVAVLVGVNLCVIGILLHNWKGKPSMTHSLNLADSLLLPSAPIRAT 84
Db 46 LIPVLVAVLVGVNLCVIGILLHNWKGKPSMTHSLNLADSLLLPSAPIRAT 112
QY 85 AVSKSVVDLGLWFCVK-----SSDWFHTCMAAKSLTIIVVAVCFMVASDPKQVSHNYT 134
Db 103 QNALSYPPFGSLMCLWMAVDGNGQFTSLELLIIVVAVCFMVASDPKQVSHNYT 161
QY 135 SIHNYTWSVLVAITVAVSLPLPEWFFSTIRHHEGVEMCLVDVPAVAEEMFSGKLYP 194
Db 162 -----TVSAAVVAVASAVVLEVVVFGV--FRGMSCTCHMWPEPAAPAGFIIYTA 211
QY 195 LLAFLGLPFFASFFWRAVDQCKRGTKT---QNIENQIPSKQVTVMLGIAIISALLNL 251
Db 212 ALGFFGLVAVLVVAVSLPLPEWFFSTIRHHEGVEMCLVDVPAVAEEMFSGKLYP 271
QY 252 PEWVAWLWHLKAAGPAPQ-----GFIALSOVLMFSSISANPLIFLVMSEERGLKV 307
Db 272 PEVYVNI-----VNVVCLPEEPFAFFGLYFLVAVLPAVASCANILYGLFELYPFA 325
QY 308 WKWMLTKKPTVSESOETFAKNSGLTDKVPSPESPASIDPEKFPSPSSCKGK 361

Query Match 10.7%, Score 231; DB 2; Length 407;
Best Local Similarity 22.18; Pred. No. 7.3e-11;
Matches 86; Conservative 80; Mismatches 159; Indels 64; Gaps 13;

QY 22 WETIIFALLVAVTIV-GEVGNLCVIGILLHNWKGKPSMTHSLNLADSLLLPSAP 80
Db 30 WQIVLWAAATVIVVTSVGVNVMWML--AHKRMETVTNYFLVNLIAFAEASMAAFNTV 87
QY 81 IPATAYSKVVDLGLWFCVKSSDWFHTCMAAKSLTIIVVAVCFMVASDPKQVSHNYT 140
Db 88 VFTTAVTIREWYVGLFYCKFNFFPIAAVAVPASIYMTAVAPDRYMAIIHPL-QPRLSATA 146
QY 141 IWSVLVAITVAVSLPLPEWFFSTIRHHEGVEMCLVDVPAVAEEMFSGKLYP----- 193
Db 147 TKWICVIVLWALLAFPPQGYISTTETTPGRVWCWMEWSPHPDK--IYEKVHICVTVL 203
QY 194 ----PLAFLGLPFFASFFWRAVDQCKRGTKTQNLNQLRSKQVTVMLGIAIISALLNL 248
Db 204 IYFLPLVLVIGYATVVGITLWAS-----RIPGSDSDRYHEQVSAKKVVKWIVVCTFAI 259
QY 249 LWLPEWVAWLWY-----HLKAAGPAPQGFIALSOVLMFSSISANPLIFLVMSEERGLKV 303
Db 260 CWLPHIFELLVPINFLYK---KFIQCVYLAIMWLAM-SSTMYNPFIYCLINDRPLFG 315
QY 304 LKGVWV-----WMLTKKPTVSESOETFAKNSGLTDKVPSPESPASIDPEKFPSPSSCKGK 361
Db 316 FPAFFPCPFISAANVEGLEMYSTYFQTGGSVYKVSLETITIS-----TVVGAHEEDPEE 371
QY 337 VPSPEPASIPPEKFPSPSSCKGKTEKA 365
```


QY 51 NAWKGKPSMIHS---LILNLSLADLSLLLFSAIRATAYSKSVWELGWPFVCKSSWFIH 106

Db 348 KPFPAGEKPAFRW 360

RESULT 15

QC7319

probable allatostatin receptor-2 fruit fly (*Drosophila melanogaster*)

C:Species: *Drosophila melanogaster*

C:Date: 08 Sep 2000 #sequence_revision 16 Sep 2002 #rev_change 02-Aug 2002

C:Accession: JC7319

R:Lenz, C.; Williams, M.; Grimmelikhuijzen, C.J.P.

Biochem. Biophys. Res. Commun. 273, 571-577, 2000

A:Title: Molecular cloning and genomic organization of a second probable allatostatin receptor, allatostatin receptor-2, from *Drosophila melanogaster*

A:Reference number: JC7319

A:Accession: JC7319

A:Molecule type: mRNA

A:Residues: 1-357 <LEN>

A:CROSS-references: GB:AF25352

C:Comment: This receptor, belonging to the insect allatostatin neuropeptide family, which is a transmembrane glycoprotein.

C:Genetics:

A:Gene: dar-2

A:Map position: right arm of chromosome 3, 98D-E

A:Introns: 180/3; 273/3; 326/3

C:Superfamily: endothelin receptor B

C:Keywords: extracellular protein; glycoprotein, neuropeptide; transmembrane protein

Query Match 10.1%; Score 218; DB 2; Length 357;

Best Local Similarity 25.1%; Pred No. 6 Re-10;

Matches 78; Conservative 57; Mismatches 132; Indels 44; Gaps 11;

QY 13 GYLPDSQDWRTIIFALLVAVCLVGVGNLCVIGILLHNWKGKPSMIHSLILSLADLSAP 72

Db 35 GTLP-----W--IVGFFFGVIAITGFGGLLVWVWF--EMSESTNEMTAAADL 85

QY 73 SLLLSAPIRATAYSKSVNDLGMFVCKSDWFIHFCMAAYSLTIWVAVVPMVASDP 130

Db 86 MFVILCIPTATIDYVYVYWPYGRFWRSCVQLIVTATASIVTLVMSIDRFLAVVHPIR 145

QY 131 AKQVSHRYTIKSLVVAIWTVASLLPLPEWFFSTIPHHGEMCLVDVPA 180

Db 146 SRMRTENITLAI-VTLVIVLVWSVPVAFTHDV--VDEYAKERTTYEMCT 195

QY 181 -VAEEFMS--MECKLYPLAFGLPLFFAGFYEWPAVDCQYFSTYKLENQIES VQVT 236

Db 196 FTINDFLGRTYVYVYFISYLLPLMLLSULVEMIMELAPSTVPMKFFVLFEEVTV 255

QY 237 VMLLSAIIKALLKEEWVAVLWVHLEAGAPAPGFIAL--SOVLMESISSANPL 291

Db 256 RLVVVVVIATASIMLPVQDILL--LKSLLVIEINTLEKLVLTATLTAISSCTHRL 311

QY 292 IFLVMSEEFRE 302

Db 312 LYAPLSENFEE 322

Search completed: January 28, 2003, 11:51:57

Job time : 23 secs

QY 22 WRTIIPALLVAVCLV GFVGNLCVIGILLHNWKGKPSMIHSLILSLADLSLLESAP 80

Db 30 WOVLVMAAAATVIVVTSVGVNVMWIIIL--AHKRMETVTNYFLVNLAFAPASAAFNTV 87

QY 81 IPATAYSKSVMLGMFVCKSDWFIHFCMAAYSLTIWVAVVPMVASDPAKQVSIHNYT 140

Db 98 VNSTVAVRHETVYGLFYCFHFFPIAVFASIVSMTAVADPVMYAIHPL-QPPLSATA 146

QY 141 INSVLVVAIWTVASLLPLPEWFFSTIRHHGEMCLVDVPAVAEFPMSMGKLY----- 193

Db 147 TVVIVCVHVIALLAFPGQYVSTTETMPSRVVCMIEWP---EHNKIYKVIHCVTVI 203

QY 194 -----PLLAFGLPLFAFVFWPAVQCFPGFTYQNLPNQIPSKQVTVMLLSIAIIS-AL 248

Db 204 IYFPLLVLYGYATVVVGIILWAS-----EIPGDSSDRYHEQVSAKRVKVMIVVVCTEAI 259

QY 249 LMLPEWVAMLVWV-----HLKAGAPAPGFIALSOVLMFSSANPLIFLVMSEEBREG 303

Db 260 CWLFFHIFELLVINDLYLK--KFIQVYLAIMWLAM-SSTMYNPITYCCLNDRFLG 315

QY 304 LKGVWK-----MMITKKPPTVSESQETPAGNSEGLPK 336

Db 316 FRIAFRCCEFISAGDEGLEMKSTRYLQGVYKVSRLTITIS---TVVGAHEERPED 371

QY 337 VPSPEPASIPKEKPSPPSSGKGKTE 363

Db 372 GPV ATPSSDLTNSAFSSPSDSKTMTE 397

RESULT 14

A34916

neurokinin 3 receptor rat

N:Alternate names: neurotensin K receptor; NK-3 receptor

C:Species: *Rattus norvegicus* (Norway rat)

C:Date: 22-Jan 1993 #sequence_revision 22-Jan-1993 #text_change 19-May-2000

C:Accession: A34916

R:Shigemoto, R.; Yokota, Y.; Tsuchida, K.; Nakanishi, S.

J. Biol. Chem. 268, 423-426, 1993

A:Title: Cloning and expression of a rat neurotensin K receptor cDNA.

A:Reference number: A34916, M312 96116113, PMID 8154106

A:Accession: A34916

A:Molecule type: mRNA

A:Residues: 1-452 <SHI>

A:CROSS-references: JN:J05461, JN:J05462, JN:J05463

C:Superfamily: neurokinin 1 receptor

C:Keywords: 3 protein-coupled receptor; glycoprotein; membrane protein

Query Match 10.1%; Score 201; DB 2; Length 452;

Best Local Similarity 24.9%; Pred No. 5.3e-10;

Matches 78; Conservative 57; Mismatches 132; Indels 46; Gaps 11;

QY 22 WRTIIPALLVAVCLVGFVGNLCVIGILLHNWKGKPSMIHSLILSLADLSLLESAP 80

Db 70 WRIALWSLAYGLVAVAVFGLNIIWIIIL--AHKRMETVTNYFLVNLAFSDASVAAFNTL 127

QY 81 IPATAYSKSVMLGMFVCKSDWFIHFCMAAYSLTIWVAVVPMVASDPAK-QVSIHNY 139

Db 128 INFIVGLHSEWYFGANYCRFQNFPIATAVPASIVSMTAIAVDRYMAIIDPLKPLRSATAT 187

QY 140 TWSVLVAIWTVASLLPLPEWFFSTIRHHGEMCLVDVPAVAEFPMS-----MECKLY 193

Db 188 KTF-VIGSIWILAFLLAFPOQLYKIKVMPGRTLCYVQWPEGKQHTYTHIIVILVYCF 245

QY 194 PLLAFGLPLFAFVFWPAVQCFPGFTYQNLNQPISKQVTVMLLSIAIIS-ALL 249

Db 246 PLLIMGVTVTIYGIITLWGEIPGDTCDK-----YHEQLKAKRKVKVMIVVVTFAIC 298

QY 250 WLPEWV-----AWLWVHLEKAGAPPGFIALSOVLMFSSANPLIFLVM 297

Db 299 WLFYHVFYILTAYQQLNFWKYI-----QQVYLA-SFWLAMSSTMYNPITYCCLN 347

QY 298 EPEFEGKGVWVW 310

PPSITE: PSSGQF2; G PROTEIN RECEPTOR FL 1; 1;
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 Multigene family
 FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL)
 FT TRANSMEM 28 48 1 (POTENTIAL)
 FT DOMAIN 29 59 2 (POTENTIAL)
 FT TRANSMEM 60 80 2 (POTENTIAL)
 FT DOMAIN 81 98 3 (POTENTIAL)
 FT TRANSMEM 99 120 3 (POTENTIAL)
 FT DOMAIN 121 140 4 (POTENTIAL)
 FT TRANSMEM 141 161 4 (POTENTIAL)
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Db 155 VGFVWALSIAMASVAVYQRLFHDSNQTFCEWHP-----NQLHKKAYVWCTFVGYL 208
 QY 200 LPLFAFSEYFEAYDQCFFCTKQNLNPNQIPSPQVTVMLISIAISALLWLPWVAWLW 259
 Db 200 LPLILLICFYAKVLLHLHK-LKMSKSEASKYTAQTIVLVVVVGGISWLPHHVHLW 267
 QY 260 VMLHKAAGFAFPQGP-ALSOVLMEFISANPLIFLVMSSEFPGLKGVKWMVITKPP 317
 Db 268 AEF--GAPLTFASFFFRITAHCLAYSNSVNPFIYAPLSENFPRKAYQVFKCRV----- 320
 QY 318 TVESQETIAGSEGLPKVSEES 342
 Db 321 ----CNESPHGDAKE-KNRIDTFPS 340

RESULT 3
 GALR_MOUSE STANDARD; PRT, 348 AA.
 AC P56479;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Galanin receptor type 1 (GALR1-R) (GALR1).
 GN GALP1 OP GALNP1 OP GALNP
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97415411; PubMed=9271210;
 RA Wang S., He C., Maguire M.T., Clemmons A.L., Purrier P.E., Guzzi M.F.,
 PA Strader C.D., Parker E.M., Rayne M.L.;
 RT "Genomic organization and functional characterization of the mouse
 Galr1 galanin receptor";
 RL FEBS Lett. 411:225-230(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RX MEDLINE=98035873; PubMed=9367674;
 PA Jacky A.S., Webb G.C., Liu M.L., Kofler E., Hort V.J., Fathi Z.,
 RA Bortema C.D.K., Shine J., Iismaa T.P.;
 RT "Structural organization of the mouse and human GALR1 galanin
 receptor gene";
 RT mouse gene";
 FL Genomics 45:430-438(1997).
 CC -!- FUNCTION: RECEPTOR FOR THE HORMONE GALANIN. THE ACTIVITY OF THIS
 RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE CYCLASE
 ACTIVITY.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- PTM: THREE CYSTEINE RESIDUES ARE FOUND IN THE C-TERMINUS, AT LEAST
 ONE OF WHICH MAY BE PALMITOYLATED (BY SIMILARITY)
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Y15004; CA475237.1;
 CC EMBL; J30657; A4887748.1;
 CC EMBL; U90655; A4887748.1; JOINED.
 CC EMBL; U90656; A4887748.1; JOINED.
 CC MGR; M31:1096364; Galr1
 CC InterPro; IPR000276; GPCR_Phosphn
 CC Pfam; PF00001; 7tm_1; 1
 CC PRINTS; PP0037; GP3PHPC0RQPSN.
 CC PROSITE; PS00017; G_PROTEIN_RECEP_F1_1; 1

DP POSITE; PS00017; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Lipoprotein; Palmitate.
 FT DOMAIN 1 34
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 35 55
 FT DOMAIN 56 70
 FT TRANSMEM 71 91
 FT TRANSMEM 92 109
 FT TRANSMEM 110 131
 FT TRANSMEM 132 151
 FT TRANSMEM 152 172
 FT TRANSMEM 173 197
 FT TRANSMEM 198 218
 FT TRANSMEM 219 247
 FT TRANSMEM 248 268
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 FT TRANSMEM 271 291
 FT TRANSMEM 292 319
 FT TRANSMEM 320 348
 FT CARBOHYD 12 12
 FT CARBOHYD 182 182
 FT CARBOHYD 183 183
 FT DISULFID 108 186
 FT LIPID 319 319
 SQ SEQUENCE 348 AA, 39114 MW, 6522752BAAI9F9A CRC64;

Query Match 12.4%; Score 269; DB 1; Length 348;
 Best Local Similarity 28.3%; Pred. No. 6.8e-11;
 Matches 87, Conservative 54, Mismatches 128, Indels 39, Gaps 14;

QY 36 VGFVGNLCVIGILLHNAWKGP-SMHSILNLSLADLSLLFSAPIRATAYSKSVWDLS 94
 Db 46 MGVLGNSLVITVLARSK-PGKPRSTTNLFILNLSIADLAVLLFCIFFCATVVALPTWVG 104
 QY 95 WFKVCKSSDFHIFHCMAKSLTIVVAKVCFMYASPAKQVSI-HNYTWSLVA----- 147
 Db 105 AFICK-----FIH-----YFTVSMVSIPTLAAMSVDPIVAIVHSPSSSIPVSRNALLS 165
 QY 148 ---IWTVAS-LPLPEWFFSTIRHGEVE-MCLVDVPAVAEEFMSFGKLYPL--LAFG-- 199
 Db 156 VGFVWALSIAMASVAVYQRLFHDSNQTFCEWHP-----NQLHKKAYVWCTFVGYL 208
 QY 200 LPLFAFSEYFMPAYQCYKPGTGTQNLNPNQIPSPQVTVMLISIAISALLWLPWVAWLW 259
 Db 210 LPLILLICFYAKVLLHLHK-LZMSKSEASKYTAQTIVLVVVVGGISWLPHHVHLW 269
 QY 260 VMLHKAAGFAFPQGP-ALSOVLMEFISANPLIFLVMSSEFPGLKGVKWMVITKPP 317
 Db 268 AEF--GAPLTFASFFFRITAHCLAYSNSVNPFIYAPLSENFPRKAYQVFKCRV----- 320
 QY 318 TVESQES 324
 Db 327 R SETKE 332

RESULT 4
 GALR_MOUSE STANDARD; PRT, 372 AA.
 AC O08726;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Galanin receptor type 2 (GALR2-R) (GALR2).
 GN GALR2 OR GALNR2.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hypothalamus;
 EX MEDLINE=97261892; PubMed=9108306;
 PA Howard A.D., Tan C., Shiao L.L., Ralyha O.C., McKee K.K.,
 PA Weinberg D.H., Feighner S.D., Cascieri M.A., Smith P.G.,

RA McGovern P., Mahle C.D., Sutherland G.P., Iismaa T.P.,
 RA Dickenson P.E., Zimanyi I.A.,
 RT "Molecular characterization, pharmacological properties and
 RT chromosomal localization of the human GALF2 galanin receptor.",
 RL Brain Res. Mol. Brain Res. 58:156-169 (1998).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9004861; PubMed=9930121;
 RA Kolakowski L.F. Jr., O'Neill G.P., Howard A.D., Roussard S.P.,
 RA Sullivan K.A., Feighner S.D., Sawdzargo M., Nguyen T., Kargman S.,
 RA Shiao L.-L., Hreniuk D.L., Tan C.P., Evans J., Abramovitz M.,
 RA Chahrouh A., George R., Ng G., Jostes M.P., Charlan A.,
 RA Khoshdel H., George S.P., Smith P.G., Cowd R.P.;
 RT "Molecular characterization and expression of cloned human galanin
 RT receptors GALR2 and GALR3.",
 RT J. Neurochem. 71:2239-2251 (1999)
 CC -1- FUNCTION: RECEPTOR FOR THE HORMONE GALANIN AND FOR GALR. THE
 CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT ACTIVATE
 CC THE PHOSPHOLIPASE C/PROTEIN KINASE C PATHWAY (VIA GQ) AND THAT
 CC INHIBIT ADENYL CYCLASE (VIA Gi)
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY WITHIN THE CENTRAL
 CC NERVOUS SYSTEM IN BOTH HYPOTHALAMUS AND HIPPOCAMPUS. IN PERIPHERAL
 CC TISSUES, THE STRONGEST EXPRESSION WAS OBSERVED IN HEART, KIDNEY,
 CC LIVER, AND SMALL INTESTINE.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 CC EMBL: AF040530; AAC39634 1;
 CC EMBL: AF080586; AAO08671.1 1;
 CC EMBL: AF058762; AAC18118.1 1;
 CC EMBL: AF042782; AAC36587 1;
 CC Genew: HMCN:4133; GALR2.
 CC MIM: 601691;
 CC InterPro: IPR000226; GPCR_Phodpsn
 CC Pfam: PF00003; 7tm_1; 1;
 CC PRINTS: P80037; GPCRPHODPSN
 CC PROSITE: PS00237; G-PROTEIN RECP FL 1; 1;
 CC PROSITE: PS0262; G-PROTEIN RECP FL 2; 1;
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC Multigene family.
 CC DOMAIN 1 28
 CC TRANSMEM 29 43
 CC DOMAIN 50 60
 CC TRANSMEM 61 81
 CC DOMAIN 82 99
 CC TRANSMEM 100 121
 CC DOMAIN 122 141
 CC TRANSMEM 142 162
 CC DOMAIN 163 187
 CC TRANSMEM 188 208
 CC DOMAIN 209 237
 CC TRANSMEM 238 258
 CC DOMAIN 259 260
 CC TRANSMEM 261 281
 CC DOMAIN 282 387
 CC CARBOHYD 2 2
 CC CARBOHYD 11 11
 CC DISULFID 98 175
 CC SEQUENCE 387 AA; 41300 MW; C522FCH91E53C47E CPO64;
 Query Match 12.2%; Score 265; DB 1; Length 387;
 Best Local Similarity 26.7%; Pred. No. 1,4e-10;
 Matches 95; Conservative 53; Mismatches 154; Indels 26; Gaps 9;
 CC 12 GGYLPSDSQDWPTIIPALLVAVTGVFVNIQVIGIILHNWAKGKPFMSHIGIHLINSLAD 71

DB 19 GQWHPK...AVTFLIPALFLVTVNTVLAVLPQS...CAUSTMFLINQVAD 71
 QY 72 LSLLSLSALPATAKSKVWDGNFVKSSDNFIHTMAKSLTINNVAVTINASDA 131
 DB 72 LQFIQCVPPQATVITDQWFGSLCKAVHFLIFLTHASSFTLAAVSRLRYLAIRYL 131
 QY 132 KQVSIHRYITWGVIVA...IWTVASLLFLPEWFFSTIRHIE...GVEMCVTVFAVAEEM 190
 DB 132 HSPFLR...TFRNLAAGLWGLSLFSGF...VLSYVPASLHANTVHANSAPESAM 190
 QY 187 S...MFGKYLALAFSLFLFASTFWAYACCHESCTFTHEMCTSEPTVWMAEL 141
 DB 188 DITTFVESVILPVNLGLTVAPTLIPYLPVAVDPV...AAGSGASPAF...EAVTWEL 141
 QY 243 ALLSALLWLFSEWAKLVWMLFAAGFAPL...GFALSLVLMFLLSNAHLILINLEEEER 192
 DB 242 AALFCTQWPHHALICVWFSGQFFLTPTATYALRLCHLSVYANGSCVFTYVALVAFHFR 192
 QY 303 GLGVWFWMTTPPTVS 320
 DB 302 GPETICAGLLGPAPGRAS 319
 RESULT 6
 GALR HUMAN STANDARD, PFT, 349 AA.
 ID P47211.
 AC 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Galanin receptor type 1 (GALR1) (GALF1).
 GN GALF1; P. GALN1; P. GALN1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Melanoma;
 RX MEDLINE=95024044; PubMed=7524088;
 RA Habert-Ortoli E., Amiranoff B., Loquet I., Laburthe M.,
 RA Mayaux J.-F.;
 RT "Molecular cloning of a functional human galanin receptor.",
 PL Proc. Natl. Acad. Sci. U.S.A. 91:9780-9783 (1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Ross P.C.;
 RC Submitted (MAR 1995) to the EMBL/GenBank/CCDC databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Small intestine;
 RX MEDLINE=98086300; PubMed=9425310;
 RA Lorimer D.D., Markowski K., Penya P.V.;
 RT "Cloning, chromosomal location, and transcriptional regulation of the
 RT human galanin 1 receptor gene (GALN1R).",
 PL Biochem Biophys Res. Commun. 241:558-564 (1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99035873; PubMed=9367074;
 RA Jacoby A.S., Webb G.C., Liu M.L., Kofler R., Hart V.J., Fathi Z.,
 RA Berman C.P., Shino T., Iismaa T.P.,
 RT "Structural organization of the mouse and human GALF1 galanin
 RT receptor genes (Galn1 and GALN1) and chromosomal localization of the
 RT mouse gene.",
 RT Genomics 45:442-458 (1997).
 CC -1- FUNCTION: RECEPTOR FOR THE HORMONE GALANIN. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE CYCLASE
 CC ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- PTM: THREE CYSTEINE RESIDUES ARE FOUND IN THE C-TERMINUS, AT LEAST
 CC ONE OF WHICH MAY BE PALMITOYLATED.

FT DOMAIN 258 259 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 260 280 7 (POTENTIAL).
 FT DOMAIN 281 370 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 6 6 N-LINKED (GLCNAC...) (POTENTIAL).
 FT DISULFID 95 172 BY SIMILARITY.
 FT DOMAIN 308 308 PALMITATE (BY SIMILARITY).
 FT LIPID 218 225 POLY-ALA.
 FT CONFLICT 54 54 R -> S (IN REF. 3).
 FT CONFLICT 127 127 R -> Q (IN REF. 2).
 FT CONFLICT 183 183 A -> P (IN REF. 2).
 FT CONFLICT 311 311 R -> C (IN REF. 2).
 SQ SEQUENCE 370 AA; 40410 MW; CESB39B6147AFAD4 CRC64;

 Query Match: 12.0%; Score 261; DB 1; Length 370;
 Best Local Similarity 24.4%; Pred. No. 2 4e 10;
 Matches 87; Conservative 53; Mismatches 155; Indels 60; Gaps 12;

 QY 26 IFALLVAVCVGVGNLCVIGILH...NAWKCKFSMIHSLIINLSLADLSLLFSAPIR 92
 DB 20 VFVIFALIFLGMVGNGLVAVLLOQFSAMQEFRTTDLFILNLAVADLCFLCCVFPQ 79

 QY 83 ATAYSKSVWELQWFKVCKSSDFHTCNAAKSLTVVVAKVCVPMVSDPAKQVSIHN-VTI 141
 DB 80 AAVITLDANLFGAFVCKTVHLLIYLTMYASSFTLAASVLDRLVAVHPHLPSPALTPRNA 139

 QY 142 WSVLVAITWVASLLPPEW FFSTIRHHEGVEMCL...-VDVPAVAEPEFMSMEG 190
 DB 140 RAAVGLVWLLAALFSAFAPYLSYGTGVR-YGALELCVPWEDARRALDVATFAA-----G 192

 QY 191 KLYPL-----LAFGLPFFASFYFWPAVDQCKKGTQNTLQNLQIRSKVTVMLSTATIS 246
 DB 193 YLLPVAVVSLAYGPTLCF-----LMAAVGPA--GAAAEAPPPATGPAGRAM-LAVAALY 244

 QY 247 ALLMLPWWVWVWHLKAGAPPAPOGFIALSOVLMSISSANPLIFLWMSSEFPEGLK 306
 DB 245 ALCWGPHHALILCFWYGRFAFSTATYACRLASHCLAYANSCNLPVYSLASHFFRPFRR 304

 QY 307 VWKMWITKKPTVSESQETAGN-----SEGLPKVPSPSPASIPKPEKP 352
 DB 305 LW.....PCGPHPHHHHPALPFPVCPASSGCPAGVPGDARP 343

RESULT 8 GALT MOUSE

ID GALT MOUSE STANDARD; PRT; 370 AA.
 AC O88853;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Galanin receptor type 3 (GAL3-R) (GALR3).
 GN GAL3 OR GALR3.
 OS Mus musculus (Mouse).
 OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
 OC Mammalia, Eutheria, Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 PP SEQUENCE FROM N A
 RC STRAIN=129/SV;
 RA Kolakowski L.F. Jr., O'Neill G.P., Howard A.D., Broussard S.R.,
 RA Sullivan P.A., Feigelson S.D., Sawzdargo M., Nguyen T., Yargman S.,
 RA Shiao L.-L., Hreniuk D.L., Tan C.P., Evans J., Abramovitz M.,
 RA Chateaufort A., Coulombe N., Ng G., Johnson M.P., Tharian A.,
 RA Khoshdel H., George S.P., Smith R.G., O'Dowd B.F.,
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: RECEPTOR FOR THE HORMONE GALANIN.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF042783; AAC36588.1; -;
 CC MGD; MGI:1329003; Galr3.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm1; 1.
 DE PRINTS; PR00237; GPCRPHODOPSIN.
 DE PROSITE; PS00237; G-PROTEIN RECP F1_1; 1.
 DE PROSITE; PS00237; G-PROTEIN RECP F1_2; 1.
 DE G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Lipoprotein; Palmitate.
 KW EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 1 20
 FT TRANSMEM 21 41 1 (POTENTIAL)
 FT DOMAIN 42 57 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 58 78 2 (POTENTIAL)
 FT DOMAIN 79 96 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 97 118 3 (POTENTIAL)
 FT DOMAIN 119 138 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 139 159 4 (POTENTIAL)
 FT DOMAIN 160 184 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 185 205 5 (POTENTIAL)
 FT DOMAIN 206 236 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 237 257 6 (POTENTIAL)
 FT DOMAIN 258 259 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 260 280 7 (POTENTIAL)
 FT DOMAIN 281 370
 FT CARBOHYD 6 6
 FT DISULFID 95 172
 FT LIPID 308 308
 FT PALMITATE (BY SIMILARITY).
 FT DOMAIN 313 318 POLY-ALA.
 FT POLY-HIS.
 SQ SEQUENCE 370 AA; 40390 MW; D387A2FCB6D28E18 CRC64;

 Query Match: 12.0%; Score 260.5; DB 1; Length 370;
 Best Local Similarity 24.4%; Pred. No. 2 6e-10;
 Matches 87; Conservative 54; Mismatches 154; Indels 61; Gaps 12;

QY 26 IFALLVAVCVGVGNLCVIGILH...NAWKCKFSMIHSLIINLSLADLSLLFSAPIR 92
 DB 20 VFVIFALIFLGMVGNGLVAVLLOQFSAMQEFRTTDLFILNLAVADLCFLCCVFPQ 79

 QY 83 ATAYSKSVWELQWFKVCKSSDFHTCNAAKSLTVVVAKVCVPMVSDPAKQVSIHN-VTI 141
 DB 80 AAVITLDANLFGAFVCKTVHLLIYLTMYASSFTLAASVLDRLVAVHPHLPSPALTPRNA 139

 QY 142 WSVLVAITWVASLLPPEW FFSTIRHHEGVEMCL...-VDVPAVAEPEFMSMEG 190
 DB 140 RAAVGLVWLLAALFSAFAPYLSYGTGVR-YGALELCVPWEDARRALDVATFAA-----G 192

 QY 191 KLYPL-----LAFGLPFFASFYFWPAVDQCKKGTQNTLQNLQIRSKVTVMLSTATIS 246
 DB 193 YLLPVAVVSLAYGPTLCF-----LMAAVGPA--GAAAEAPPPATGPAGRAM-LAVAALY 244

 QY 247 ALLMLPWWVWVWHLKAGAPPAPOGFIALSOVLMSISSANPLIFLWMSSEFPEGLK 306
 DB 245 ALCWGPHHALILCFWYGRFAFSTATYACRLASHCLAYANSCNLPVYSLASHFFRPFRR 304

 QY 307 VWKMWITKKPTVSESQETAGN-----SEGLPKVPSPSPASIPKPEKP 352
 DB 305 LW.....PCGPHPHHHHPALPFPVCPASSGCPAGVPGDARP 343

 RESULT 9
 GALT HUMAN
 ID GALT HUMAN STANDARD; PRT; 368 AA.
 AC O60755;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Galanin receptor type 3 (GAL3-R) (GALR3)
 GN GALR3 OR GALNP3
 OS Homo sapiens (Human)

RA Zhan M., Zhang G., Chissee S., Murray J., Miller N., Minx P.,
 RA Fulton R., Johnson D., Benis G., Bentley D., Bradshaw H., Bourne S.,
 RA Cerdes M., Du Z., Fullon L., Goela D., Graves T., Hawkins J.,
 RA Hinds K., Kemp K., Lathrelle P., Layman D., Ozersky P., Rohlfing T.,
 RA Korf I., Bedell J.A., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
 RA Schell P., Hillier L., Hillier L., Mardis E., Waterston R., Wilson R.,
 RA Emanuel B.S., Shaikh T., Kulkarni H., Saitta S., Budarf M.L.,
 RA McDermid H.E., Johnson A., Wong A.C.C., Kortow B.E., Edelmann L.,
 RA Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kieda D.,
 RA Seroussi E., Franssen I., Tapia I., Bruder C.E., O'Brien K.P.,
 RA Wilkerson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
 RA Tilahun Y., Wright H.,
 RT "The DNA sequence of human chromosome 22";
 RL Nature 402:489-495(1999).
 CC -1 FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
 CC COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
 CC ADENYLYL CYCLASE.
 CC -1 SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1 TISSUE SPECIFICITY: BRAIN, PITUITARY AND PANCREAS.
 CC -1 SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC or send an email to license@isb-sib.ch).
 DR EMBL; M96738; AAA60592.1; -;
 DR EMBL; 282188; CAB45283.1; -;
 DR PIR; S32501; S32501.
 DR PIR; A46226; A46226.
 DR HSP; P34996; IIDD.
 DR Genew; HGNC:11332; SSTR3.
 DR MIM; 182453; -;
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multi-gene family; Polymorphism.
 FT DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 44 69 1 (POTENTIAL).
 FT DOMAIN 70 79 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 80 101 2 (POTENTIAL).
 FT DOMAIN 102 116 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 117 138 3 (POTENTIAL).
 FT DOMAIN 139 161 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 162 181 4 (POTENTIAL).
 FT DOMAIN 182 205 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 206 231 5 (POTENTIAL).
 FT DOMAIN 232 257 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 258 279 6 (POTENTIAL).
 FT DOMAIN 280 303 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 304 316 7 (POTENTIAL).
 FT DOMAIN 317 418 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 17 17 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 30 30 N-LINKED (GLCNAC...) (POTENTIAL).
 FT DISULFID 116 191 BY SIMILARITY.
 FT DOMAIN 346 360 GLU-RICH (ACIDIC).
 FT VARIANT 411 411 S->T (IN DBSNP:229568).
 SQ SEQUENCE 418 AA; 45847 MW; 1227095F801190C4 CRC64;
 Query Match 10.6%, Score 229; DB 1; Length 418;
 Best Local Similarity 23.4%; Pred. No. 3, 4e-08;
 Matches 83; Conservative 63; Mismatches 160; Indels 48; Gaps 11;
 Q7 25 IIPALLVAIVLVGVNIGVIGILHNNAWKPKPMHSLIINLSLADISLLFSPAPIRAT 84
 DB 46 LIPIVLVGVNIGVIGILHNNAWKPKPMHSLIINLSLADISLLFSPAPIRAT 102

QY AS AVSKSVMDLWPFVCF----SSWPHITWAAVGLTIVYAKVTEWVADEAFV 134
 DB 103 QNALSYWPFGLMCLMCLMAVDGINQFISICLTVMVDRIYLVHPTESAKWRAPAR 161
 QY 135 SIHNYTINSVLVAITVASLPLPEWPFSTRHHEGVEMCIDVDPAVAEEFMSFGKLYP 194
 DB 162 -----CVSAAVWVASAVVLVWVFGV--PRGMSCTHMQWPFPAAMAFAGITVA 211
 QY 195 LIAFLGLPFFASFVFWPAYDCKYKPTKT---QVLEQIPKSVQVYTWMLSLALCALNL 251
 DB 212 ALGPFGLVIVICLYLIVVKSAGFVWAPSQCPEPPFVPMVAVVAVLVQWM 271
 QY 252 PEWIAWLWVHKAAGRAPPO---GFIALSQVLMFRTSSAMFLFTVMGFEEFELEEV 307
 DB 272 PFYVNI---VTVVCLPEEFVAFGLYLVVALFVANSANFLYGLSLYKPAQGR-- 425
 QY 308 WKWMLTKPPTVSFSQETPAGNSGLPKVPSPEPASIEKEKPSFSSGKX 341
 DB 326 ---RVLLFPSPVTSQETVGP---PEFTEPDE---PEFTEPDEPDEPDE 368
 RESULT 13
 ID NK1R_MOUSE STANDARD; PRT; 407 AA.
 AC P30548;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Substance-P receptor (SPR) (NK-1 receptor) (NK-1R).
 GN TACR1 OR TAC1R.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Intestine;
 RX MEDLINE=92137253; PubMed=13700937;
 RA Sundelin J.B., Provvedini D.M., Wahlestedt C.P., Laurell H.,
 RA Pohl J.S., Peterson P.A.;
 RT "Molecular cloning of the murine substance P and substance P receptor
 genes.";
 RL Eur. J. Biochem 203:625-631(1992).
 RN [2]
 RP SEQUENCE OF 63-290 FROM N.A.
 RC STRAIN=CBA; TISSUE=T-cell, and Brain;
 RX MEDLINE=94165478; PubMed=8120392;
 RA Cook G.A., Elliott D., Metwali A., Blum A.M., Sandoz M., Lynch R.,
 RA Weinstein J.V.;
 RT "Molecular evidence that granuloma T lymphocytes in murine
 schistosomiasis mansoni express an authentic substance P (NK-1)
 receptor.";
 RL J. Immunol. 152:1830-1835(1994).
 CC -1 FUNCTION: THIS IS A RECEPTOR FOR THE TACHYKININ NEUROPEPTIDE
 CC SUBSTANCE P. IT IS PROBABLY ASSOCIATED WITH G PROTEINS THAT
 CC ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
 CC -1 SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1 MISCELLANEOUS: THE RANK ORDER OF AFFINITY OF THIS RECEPTOR TO
 CC TACHYKININS IS: SUBSTANCE P > SUBSTANCE K > NEUREGEMIN K.
 CC -1 SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC HIGHEST TO OTHER TACHYKININS RECEPTORS.
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 CC or send an email to license@isb-sib.ch).
 DR EMBL; X62934; CAA44707.1; -;
 DB EMBL; L27828; AAM17892.1; -;

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OM protein - protein search, using sw model

Run on: January 28, 2003, 11:49:51, search time 17 seconds
(without alignments)
702.689 Million cell updates/sec

Title: US-09-828-432-3

Perfect score: 2.67

Sequence: 1 MWSFAHLRPGAGYLESTQ . . . QNTPIWEHRCGETREGVY 406

Scoring table: BLOSUM62

Gapop 10 0, Gapext 0 5

Searched: 252574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued Parents_AA+
1: /cgn2_6/prodata/1/1aa/5A_CMB rep.*
2: /cgn2_6/prodata/1/1aa/5B_CMB rep.*
3: /cgn2_6/prodata/1/1aa/5A_CMB rep.*
4: /cgn2_6/prodata/1/1aa/5B_CMB rep.*
5: /cgn2_6/prodata/1/1aa/6CTUS_CMB rep.*
6: /cgn2_6/prodata/1/1aa/6A_CMB rep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No	Score	Query Match	Length	ID	Description
1	270.5	12.5	371	4	US-08-993-088A-9
2	270.5	12.5	371	4	US-08-993-424B-9
3	269.5	12.4	346	4	US-09-199-737-5
4	269.5	12.4	346	4	US-08-993-088A-3
5	269.5	12.4	346	4	US-08-993-424B-3
6	269.5	12.4	346	4	US-09-058-333A-5
7	269	12.4	348	3	US-09-513-974R-46
8	269	12.4	348	4	US-08-993-088A-10
9	269	12.4	348	4	US-08-993-424B-10
10	269	12.4	348	4	US-08-540-650B-2
11	269	12.4	349	3	US-08-513-974R-143
12	269	12.4	372	4	US-08-665-034A-2
13	267	12.3	372	2	US-09-606-685A-8
14	267	12.3	372	4	US-08-993-088A-2
15	267	12.3	372	4	US-09-993-424B-2
16	267	12.3	372	4	US-08-665-034A-4
17	265	12.2	387	4	US-08-993-088A-7
18	265	12.2	387	4	US-08-993-424B-7
19	264	12.2	348	3	US-08-513-974B-342
20	263	12.1	370	4	US-09-199-737-2
21	263	12.1	372	4	US-08-993-088A-20
22	263	12.1	395	4	US-08-900-230-5
23	262.5	12.1	349	4	US-08-993-088A-11
24	262.5	12.1	340	4	US-08-993-424B-11
25	262.5	12.1	349	4	US-09-540-650B-6
26	262.5	12.1	349	4	US-08-693-308-2
27	262.5	12.1	351	3	US-09-513-974B-344

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28 262 12.1 370 4 US-08-993-088A-9
29 262 12.1 370 4 US-09-058-333A-2
30 259.5 12.0 427 4 US-09-199-737-4
31 259.5 12.0 427 4 US-08-993-088A-3
32 259.5 12.0 427 4 US-09-058-333A-4
33 259.5 12.0 418 1 US-07-916-749-10
34 229 10.6 418 1 US-08-417-103-10
35 227 10.5 407 5 FCT US92-06632-7
36 224.5 10.4 440 4 US-08-430-286A-9
37 224.5 10.4 451 4 US-09-420-384A-10
38 224 10.3 465 4 US-08-090-369-1
39 224 10.3 465 4 US-09-482-971-1
40 222 10.2 407 2 US-08-290-000A-6
41 221 10.2 407 1 US-08-117-065-26
42 221 10.2 407 5 FCT US92-06632-3
43 221 10.2 411 1 US-07-937-609-21
44 221 10.2 411 4 US-08-029-170-21
45 217 10.3 353 1 US-08-148-200A-2

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ALIGNMENTS

RESULT 1

US-08-993-088A-9

Sequence 9, Application US/08993088A

Patent No. 6297855

GENERAL INFORMATION:

APPLICANT: Tan, Carina

APPLICANT: Sullivan, Kathleen

TITLE OF INVENTION: SALAMIN PEPTIDE DAPIF AND

TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.

STREET: P.O. Box 2000, 125 E. Lincoln Ave.

CITY: Rahway

STATE: NJ

COUNTRY: USA

ZIP: 07065-0900

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows

SOFTWARE: FASTSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/993,088A

FILING DATE: 18-DEC-1997

CLASSIFICATION: 530

PIIOP APPLICATION DATA:

APPLICATION NUMBER: 60/033,851

FILING DATE: 27-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Heber, Sheldon C.

REGISTRATION NUMBER: 38,179

REFERENCE/DOCKET NUMBER: 19846

TELECOMMUNICATION INFORMATION:

TELEPHONE: 732 594-1958

TELEFAX: 732 594-4720

TELEX:

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 371 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-993-088A-9

Query Match: 12.5%, Score 270.5, 22.4, Length 371

Post Local Similarity: 24.7%, Pval. No. 1.3e-14

Matches: 92, Conservative: 61, Mismatches: 178, Indels: 4, Gaps: 11

QY 12 GGYLPDCCGQWPTIIPALVAVGVGVGHCVIGILLHNAMKGYPMHLSLILSLAD 71
 Db 18 GQWPE-----AVLPLEFFALIFLVGAAGRAVLAVLFGG---QAVSTTNLFLNLGVAD 70
 QY 72 LSLLESAPATAYSGVWGLQWPFYKSSDWFHTCMAAYSLTIIVVAVFVPMVSDPA 131
 Db 71 LCFILCVPEQATYITLQWVFSLLCKAVHFLILTMHASSFTLAASLDRLYLAIRYM 130
 QY 132 KQVSHNYTWSVLA--IWTVASLLPDEWFFSTIRIHGVEMLCVDPVAVAEFMSM 189
 Db 131 HSPFLP--TPNALAAIGLWGLLFLFSQYLSYSSQSLANLTVCHPAWSPAPFAMEL 188
 QY 189 ---FAYLYELLAFGLPIFASVYFPAVDQWFFPTKTONLPNCPSPQVTVMLLSIAL 244
 Db 189 QTFVFSYLLPVLIVSYTYARTLYLMTVPV-AAQSGSDPA-----PFVTPMIVIVAV 243
 QY 245 ISALLKPEFVAKWVWHLFVAAIPATQFTALGVLMFSSSARPLFLVWSEFPEEL 304
 Db 243 LFCCLWNSHALLLCVWFGPFETPATYALFILSHVSVYANSTVNFIVVALYSFHPFF 302
 QY 305 KGVWFWMTTFPTTVRSQ--ETFAVNSGLPVVPSPEP--ASTPPEFETLILKPL 360
 Db 303 PKICAGILPPAPPASGVCLAPNSHSGMLE---PESTLUTQVSEAAAGPLVPA---- 354
 QY 361 KTEVAEIPILPD 372
 Db 355 -----PALPN 359

RESULT 2

US-09-993-424B-9
 : Sequence 9, Application US/08993424B
 : Patent No. 6337206

: GENERAL INFORMATION:

: APPLICANT: Tan, Carina
 : APPLICANT: Kollakowski, Lee F, Jr
 : TITLE OF INVENTION: METSE GALANIN PEPTIDE GALT2 AND
 : TITLE OF INVENTION: NUCLEOTIDE SEQUENCES
 : NUMBER OF SEQUENCES: 18
 : CORRESPONDENCE ADDRESS:

: ADDRESSEE: Merck & Co., Inc.
 : STREET: P.O. Box 200, 126 E. Lincoln Ave.
 : CITY: Rahway

: STATE: NJ

: COUNTRY: USA

: ZIP: 07065-0900

: COMPUTER READABLE FORM

: MEDIUM TYPE: Diskette
 : COMPUTER: IBM compatible
 : OPERATING SYSTEM: Windows
 : SOFTWARE: FastSeq for Windows Version 2.0b

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/09/993,424B

: FILING DATE: 18-DEC-1997

: CLASSIFICATION: 536

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: 60/033,851

: FILING DATE: 27-DEC-1996

: ATTORNEY/AGENT INFORMATION:

: REPRESENTATION NUMBER: 14,170

: REFERENCE/DOCKET NUMBER: 19846NF2

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: 732-594-1958

: TELEFAX: 732-594-4720

: TELEX:

: INFORMATION FOR SEQ ID NO 9:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 371 amino acids

: TYPE: amino acid

: STRANDEDNESS: single

: TOPOLOGY: linear

: MOLECULE TYPE: polypeptide

US-09-993-424B-9

Query Match: 12.5%; Score 270.5; DB 4; Length 371

Best Local Similarity: 24.7%; Prod. No. 1.1e 147

Matches: 9; Conservative: 61; Mismatches: 198; Indels: 41; Gaps: 11

QY 12 GGYLPDCCGQWPTIIPALVAVGVGVGHCVIGILLHNAMKGYPMHLSLILSLAD 71
 Db 18 GQWPE-----AVLPLEFFALIFLVGAAGRAVLAVLFGG---QAVSTTNLFLNLGVAD 70
 QY 72 LSLLESAPATAYSGVWGLQWPFYKSSDWFHTCMAAYSLTIIVVAVFVPMVSDPA 131
 Db 71 LCFILCVPEQATYITLQWVFSLLCKAVHFLILTMHASSFTLAASLDRLYLAIRYM 130
 QY 132 KQVSHNYTWSVLA--IWTVASLLPDEWFFSTIRIHGVEMLCVDPVAVAEFMSM 189
 Db 131 HSPFLP--TPNALAAIGLWGLLFLFSQYLSYSSQSLANLTVCHPAWSPAPFAMEL 188
 QY 189 ---FAYLYELLAFGLPIFASVYFPAVDQWFFPTKTONLPNCPSPQVTVMLLSIAL 244
 Db 189 QTFVFSYLLPVLIVSYTYARTLYLMTVPV-AAQSGSDPA-----PFVTPMIVIVAV 243
 QY 245 ISALLKPEFVAKWVWHLFVAAIPATQFTALGVLMFSSSARPLFLVWSEFPEEL 304
 Db 243 LFCCLWNSHALLLCVWFGPFETPATYALFILSHVSVYANSTVNFIVVALYSFHPFF 302
 QY 305 KGVWFWMTTFPTTVRSQ--ETFAVNSGLPVVPSPEP--ASTPPEFETLILKPL 360
 Db 303 PKICAGILPPAPPASGVCLAPNSHSGMLE---PESTLUTQVSEAAAGPLVPA---- 354
 QY 361 KTEVAEIPILPD 372
 Db 355 -----PALPN 359

RESULT 3

US-09-199-737-5

: Sequence 5, Application US/09199737A

: Patent No. 6287788

: GENERAL INFORMATION:

: APPLICANT: Bard, Jonathan A.

: APPLICANT: Borowsky, Beth

: APPLICANT: Smith, Kelli E.

: APPLICANT: Branchek, Theresa A.

: APPLICANT: Getald, Christophe P.G.

: APPLICANT: Jones, Kenneth A.

: TITLE OF INVENTION: DNA Encoding Galanin GALT2 Peptide and Galanin Receptor

: FILE REFERENCE: 5241 C PCT US

: CURRENT APPLICATION NUMBER: US/09/199,737A

: CURRENT FILING DATE: 1998-11-25

: NUMBER OF SEQ ID NOS: 59

: SOFTWARE: Patent in Ver. 2.0 beta

: SEQ ID NO 5

: LENGTH: 346

: TYPE: PRT

: ORGANISM: Rat

US-09-199-737-5

Query Match: 12.4%; Score 263.5; DB 4; Length 346

Best Local Similarity: 27.1%; Prod. No. 1.1e 147

Matches: 88; Conservative: 60; Mismatches: 130; Indels: 47; Gaps: 17

QY 36 VGFVJNLVIGILLHNAMKGYPMHLSLILSLAD 71
 Db 45 MGVLGSLVITVLAESK POFSTTNLFLNLGVAD 70
 QY 95 WFTVSESWNTINAAAGLITVAVVETVLA 147
 Db 104 AFICK...PIH...YPTVSMVSVIFTLAAMSVDYVAIVHSRSHSVFVFAALL 164
 QY 148...IWTVASLLPDEWFFSTIRIHGVEMLCVDPVAVAEFMSM 189
 Db 155 VGFVJNLVIGILLHNAMKGYPMHLSLILSLAD 71

QY 200 LPLPASTVYFVPAVYQYKPPPTFTNTLNQKESQVTVWLLSIALISALLWPERVAMW 259
 DB 209 LPLLLICPYAVVHLHHPV LKNSVPSSEASYKKTACTVILVVVVVPOISLPHVILHW 267
 QY 260 VHLKAAAPAPQRTI--ALQVLMFSSISSAPHLIFUNVSEFFPEGLGVWMMITFYPP 317
 DB 269 LLLLCCTVAKYVHLHHPV LKNSVPSSEASYKKTACTVILVVVVVPOISLPHVILHW 267
 QY 260 VHLKAAAPAPQRTI--ALQVLMFSSISSAPHLIFUNVSEFFPEGLGVWMMITFYPP 317
 DB 269 LLLLCCTVAKYVHLHHPV LKNSVPSSEASYKKTACTVILVVVVVPOISLPHVILHW 267
 QY 318 TVSESEETAGSEGLCKVSEES 342
 DB 321 --CHESRCCAKE KRIDTPPS 340
 RESULT 4
 US-08-993-088A-3
 : Sequence 3, Application US/08993088A
 : Patent No. 6287855
 : GENERAL INFORMATION:
 : APPLICANT: Tan, Carina
 : APPLICANT: Sullivan, Kathleen
 : TITLE OF INVENTION: GALANIN RECEPTOR GALP2 AND
 : TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME
 : NUMBER OF SEQUENCES: 20
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Merck & Co., Inc.
 : STREET: P.O. Box 2000, 126 E Lincoln Ave.
 : CITY: Rahway
 : STATE: NJ
 : COUNTRY: USA
 : ZIP: 07065-0900
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette
 : COMPUTER: IBM Compatible
 : OPERATING SYSTEM: Windows
 : SOFTWARE: FASTSEQ for windows Version 2.0b
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/993,088A
 : FILING DATE: 18-DEC-1997
 : CLASSIFICATION: 530
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 60/033,851
 : FILING DATE: 27-DEC-1996
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Hebert, Sheldon O.
 : REGISTRATION NUMBER: 38,179
 : REFERENCE/DOCKET NUMBER: 19846
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 732-594-1958
 : TELEFAX: 732-594-4720
 : TELEX:
 : INFORMATION FOR SEQ ID NO: 3:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 346 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-993-088A-3

Query Match 12.4%, Score 269.5, DB 4, Length 346;
 Best Local Similarity 27.1%, Pred. No. 1.5e-14;
 Matches 89; Conservative 60; Mismatches 130; Indels 47; Gaps 15;

QY 36 VFEVENLVIGILLHNWFKPP-SMHSLLILNLSLADSLILPSAPIPATAYSVSWALG 94
 DB 45 N-VLNSGLTIVLASPP PPTFTSTNLTNLNLSLADSLILPSAPIPATAYSVSWALG 103
 QY 95 WFTVPSKFTHTMAAFSLTIWVAFVFMVASLILAFVSI HMLINQVVA 147
 DB 104 AFICK FIK --YFTVSMVSLIPLAAAGVTVVAIVHSPRSSSLFVSPNALG 154
 QY 148 -IWTVASLLPLDPWFSTISHHEVE-MCLVTVVAEEMSMFTYLYPL-LAFS- 199

DB 155 VQIEMALSIAMASVAVYQYKPPPTFTNTLNQKESQVTVWLLSIALISALLWPERVAMW 259
 QY 200 LPLPASTVYFVPAVYQYKPPPTFTNTLNQKESQVTVWLLSIALISALLWPERVAMW 259
 DB 209 LPLLLICPYAVVHLHHPV LKNSVPSSEASYKKTACTVILVVVVVPOISLPHVILHW 267
 QY 260 VHLKAAAPAPQRTI--ALQVLMFSSISSAPHLIFUNVSEFFPEGLGVWMMITFYPP 317
 DB 269 LLLLCCTVAKYVHLHHPV LKNSVPSSEASYKKTACTVILVVVVVPOISLPHVILHW 267
 QY 260 VHLKAAAPAPQRTI--ALQVLMFSSISSAPHLIFUNVSEFFPEGLGVWMMITFYPP 317
 DB 269 LLLLCCTVAKYVHLHHPV LKNSVPSSEASYKKTACTVILVVVVVPOISLPHVILHW 267
 QY 318 TVSESEETAGSEGLCKVSEES 342
 DB 321 --CHESRCCAKE KRIDTPPS 340
 RESULT 5
 US-08-993-424B-3
 : Sequence 3, Application US/08993424B
 : Patent No. 6337206
 : GENERAL INFORMATION:
 : APPLICANT: Tan, Carina
 : APPLICANT: Kolakowski, Lee P. Jr.
 : TITLE OF INVENTION: MOUSE GALANIN RECEPTOR GALP2 AND
 : TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME
 : NUMBER OF SEQUENCES: 18
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Merck & Co., Inc.
 : STREET: P.O. Box 2000, 126 E Lincoln Ave.
 : CITY: Rahway
 : STATE: NJ
 : COUNTRY: USA
 : ZIP: 07065-0900
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette
 : COMPUTER: IBM Compatible
 : OPERATING SYSTEM: Windows
 : SOFTWARE: FASTSEQ for Windows Version 2.0b
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/993,424B
 : FILING DATE: 18-DEC-1997
 : CLASSIFICATION: 536
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 60/033,851
 : FILING DATE: 27-DEC-1996
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Hebert, Sheldon O.
 : REGISTRATION NUMBER: 38,179
 : REFERENCE/DOCKET NUMBER: 19846RP2
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 732-594-1958
 : TELEFAX: 732-594-4720
 : TELEX:
 : INFORMATION FOR SEQ ID NO: 3:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 346 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-993-424B-3

Query Match 12.4%, Score 269.5, DB 4, Length 346;
 Best Local Similarity 27.1%, Pred. No. 1.5e-14;
 Matches 89; Conservative 60; Mismatches 130; Indels 47; Gaps 15;

QY 36 VFEVENLVIGILLHNWFKPP-SMHSLLILNLSLADSLILPSAPIPATAYSVSWALG 94
 DB 45 N-VLNSGLTIVLASPP PPTFTSTNLTNLNLSLADSLILPSAPIPATAYSVSWALG 103
 QY 95 WFTVPSKFTHTMAAFSLTIWVAFVFMVASLILAFVSI HMLINQVVA 147
 DB 104 AFICK FIK --YFTVSMVSLIPLAAAGVTVVAIVHSPRSSSLFVSPNALG 154
 QY 148 -IWTVASLLPLDPWFSTISHHEVE-MCLVTVVAEEMSMFTYLYPL-LAFS- 199

QY 148 ---INTVASLLPLPEPFSTIRHHEGV-MCLVDVPAVAEEMSMCKLYPL--LAFG-- 199
 DB 155 VGFALGAGAGVAVYQQLFFETGTEFWEHWP- NCHFFAYVVTFFVETW 208
 QY 200 LPLPEAFSEVPAYVQCFKFGTFTNINLPNATPSQVTVMTLSIAISALILWPEWVAMW 259
 DB 209 LPLLLICFCYAKVNLHLHK-LKMSKSEASKKTAQTVLVVVVFGISWLPHHVHLW 267
 QY 260 VWHKFAAGAPPQCFI--ALSQVLMFSISSANPLIFLVMSEEPGLKGWKMITYKPP 317
 DB 268 AEF--GAPFLTTAFSEFFITAHCTAYGNSVNTIIVAFISNFFAYKQVYKCPV..... 320
 QY 318 TVSESQETPAGNSEGLPKVPSDES 342
 DB 321 ----CNESPHGDAKE-KNRIDTPES 340

RESULT 6

US-09-058-333A-5
 ; Sequence 5, Application US/09058333A
 ; Patent No. 6144139
 ; GENERAL INFORMATION:
 ; APPLICANT: Bard, Jonathan A
 ; APPLICANT: Berowsky, Beth
 ; APPLICANT: Smith, Kelli E
 ; TITLE OF INVENTION: RNA ENCODING GALANIN GALS3 RECEPTORS
 ; TITLE OF INVENTION AND USE THEREOF
 ; NUMBER OF SEQUENCES: 55
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U S A
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1 0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/058,333A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P
 ; REGISTRATION NUMBER: 28,678
 ; PREFERENCE/COCKET NUMBER: 50741-E/JPW/ETP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212 378 0400
 ; TELEFAX: 212 301 0525
 ; INFORMATION FOR SEQ ID NO. 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 346 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; US-09-058-333A-5

Query Match 12.4%, Score 209.5, DB 4, Length 346,
 Best Local Similarity 27.1%, P-Val 1e-14,
 Matches 99, Conservative 60, Mismatches 130, Indels 47, Gaps 15,
 QY 36 VGEVGNLCYGHILHAKWQFF-SMHSUHLHSLSLLESADIPATAYFSFWOLG 94
 DB 45 MGVLGRSIVITVIRSP-PCPFSTTNLFTLRSIACAYLFCIPQATVVALFTWVLG 103
 QY 95 WFTVFSQWFIHMAAFPSITIVVAVVPMVASTAPAVQSY HRYTIVELVVA..... 147
 DB 104 AFICK----FIH-----YFTVSNLVSIFTLAASVVPVVAIVHSPPSSSLVSPNALIG 154

QY 148 ---INTVASLLPLPEPFSTIRHHEGV-MCLVDVPAVAEEMSMCKLYPL--LAFG-- 199
 DB 155 VGFALGAGAGVAVYQQLFFETGTEFWEHWP- NCHFFAYVVTFFVETW 208
 QY 200 LPLPEAFSEVPAYVQCFKFGTFTNINLPNATPSQVTVMTLSIAISALILWPEWVAMW 259
 DB 209 LPLLLICFCYAKVNLHLHK-LKMSKSEASKKTAQTVLVVVVFGISWLPHHVHLW 267
 QY 260 VWHKFAAGAPPQCFI--ALSQVLMFSISSANPLIFLVMSEEPGLKGWKMITYKPP 317
 DB 268 AEF--GAPFLTTAFSEFFITAHCTAYGNSVNTIIVAFISNFFAYKQVYKCPV..... 320
 QY 318 TVSESQETPAGNSEGLPKVPSDES 342
 DB 321 ----CNESPHGDAKE-KNRIDTPES 340

RESULT 7

US-08-513-974B-46
 ; Sequence 46, Application US/08513974B
 ; Patent No. 6114139
 ; GENERAL INFORMATION:
 ; APPLICANT: Hinuma, Shuji
 ; APPLICANT: Hosoya, Masaki
 ; APPLICANT: Fujii, Ryo
 ; APPLICANT: Ohtaki, Tetsuya
 ; APPLICANT: Fukusumi, Shoji
 ; APPLICANT: Ohji, Kazuhiko
 ; TITLE OF INVENTION: G PROTEIN COUPLED PROTEIN RECEPTOR
 ; NUMBER OF SEQUENCES: 380
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GSKF, BRONSTEIN, ROBERTO & CUSHMAN, LLP
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/513,974B
 ; FILING DATE: 14-SEP-1995
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP/085701599
 ; FILING DATE: 10-AUG-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 7-093989
 ; FILING DATE: 19-AUG-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 7 057186
 ; FILING DATE: 16-MAR-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 7-007177
 ; FILING DATE: 20-JAN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 6 326611
 ; FILING DATE: 28-DEC-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 6-270017
 ; FILING DATE: 02-NOV-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 6-236357
 ; FILING DATE: 30-SEP-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 6 236356
 ; FILING DATE: 30-SEP-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 6 189274

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; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JF 6 180273
; FILING DATE: 11-AUG-1945
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JF 6-189272
; FILING DATE: 11-AUG 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-513-974B-46

```

```

Query Match 12.4%, Score 269, DB 3, Length 348,
Best Local Similarity 28.3%, Pred. No. 1.6e-14,
Matches 87; Conservative 54; Mismatches 128; Indels 38; Gaps 14,

```

```

QY 36 VGFVGNLGVIGILLHNWAKGKP-SMIHSLIINLSLADLSLLFSAPIPATAYSKSVNCLG 94
Db 46 MVLGNSLIVITVLAPSK-PGKPPSTTNILFIINLSIADIAYLLFCIPQATVYALPTWVLG 104
QY 95 WPCVCKSSQMFHTICMAAKSLTIIVVAKVCFMYASDPAFQVGI-HNYTWSVLVA----- 147
Db 105 AFPCY----FIH-----VFETVSLVSIETLAAMSVDPYVAIVHSRPSRSI,PUVSPNALLG 155
QY 148 ---TWTVASLLPLPWFSTTPIHKGVE-MCLIVVPVAVASEPMFMPGKLYPL--LAFG-- 199
Db 156 VFTWALSTAMASPVAYHQPIFHPTDSNTPF--WEQWP-----NFIHPKAYVYVUTFEVSYL 209
QY 250 LPLFAGFVFPVAVGCTPPFCTTQNLFNQ-PSQVTVMLSTAIIGALLWLEFWAMW 259
Db 210 LFLILLTFTYAVLNHLHFK-IFMSKSESEASKYFCACTVUUVVVVFNLSLPHVWHLW 249
QY 260 VMLHPAA-PATPQGT ALSCVLMFELSSANPLIFLWSESEFELKLVNWMWATRAFI 317
Db 269 AEF--CAPLTTFASFFRITAHCLAYSSNSVNTIYAFSESEFPAVEVFFCHVCLSEF 326
QY 318 TVSESQE 324
Db 327 R-SETKE 332

```

```

RESULT 8
US-08-993-088A-10
; Sequence 10, Application US/08993088A
; Patent No. 6287855
; GENERAL INFORMATION:
; APPLICANT: Tan, Garina
; APPLICANT: Sullivan, Kathleen
; TITLE OF INVENTION: GALANIN RECEPTOR GALK2 AND
; TITLE OF INVENTION: NOCTESTIDES ENCODING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P O Box 2000, 126 E Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows

```

```

; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,088A
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/033,851
; FILING DATE: 27-DEC 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 19946
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1958
; TELEFAX: 732 594 4720
; TELEX:

```

```

; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-993-088A-10

```

```

Query Match 12.4%, Score 269, DB 4, Length 348,
Best Local Similarity 29.3%, Pred. No. 1.6e-14,
Matches 87; Conservative 54; Mismatches 128; Indels 38; Gaps 14,

```

```

QY 36 VGFVGNLGVIGILLHNWAKGKP-SMIHSLIINLSLADLSLLFSAPIPATAYSKSVNCLG 94
Db 46 MVLGNSLIVITVLAPSK-PGKPPSTTNILFIINLSIADIAYLLFCIPQATVYALPTWVLG 104
QY 95 WPCVCKSSQMFHTICMAAKSLTIIVVAKVCFMYASDPAFQVGI-HNYTWSVLVA----- 147
Db 105 AFPCY----FIH-----VFETVSLVSIETLAAMSVDPYVAIVHSRPSRSI,PUVSPNALLG 155
QY 148 ---TWTVASLLPLPWFSTTPIHKGVE-MCLIVVPVAVASEPMFMPGKLYPL--LAFG-- 199
Db 156 VFTWALSTAMASPVAYHQPIFHPTDSNTPF--WEQWP-----NFIHPKAYVYVUTFEVSYL 209
QY 250 LPLFAGFVFPVAVGCTPPFCTTQNLFNQ-PSQVTVMLSTAIIGALLWLEFWAMW 259
Db 210 LFLILLTFTYAVLNHLHFK-IFMSKSESEASKYFCACTVUUVVVVFNLSLPHVWHLW 249
QY 260 VMLHPAA-PATPQGT ALSCVLMFELSSANPLIFLWSESEFELKLVNWMWATRAFI 317
Db 269 AEF--CAPLTTFASFFRITAHCLAYSSNSVNTIYAFSESEFPAVEVFFCHVCLSEF 326
QY 318 TVSESQE 324
Db 327 R-SETKE 332

```

```

RESULT 9
US-08-993-424B-10
; Sequence 10, Application US/08993424B
; Patent No. 6337206
; GENERAL INFORMATION:
; APPLICANT: Tan, Garina
; APPLICANT: Kolarowski, Lee F., Jr.
; TITLE OF INVENTION: MOUSE GALANIN RECEPTOR GALK2 AND
; TITLE OF INVENTION: NOCTESTIDES ENCODING SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P O Box 2000, 126 E Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

```

```

? COMPUTER: IBM Compatible
? OPERATING SYSTEM: Windows
? SOFTWARE: FastSeq for Windows Version 2.0.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/98/933,424B
? FILING DATE: 18-DEC-1997
? CLASSIFICATION: 536
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 98/033,424
? FILING DATE: 27 DEC 1996
? ATTORNEY/AGENT INFORMATION:
? NAME: Hebel, Sheldon O.
? REGISTRATION NUMBER: 39,179
? REFERENCE/COCKET NUMBER: 1984CNP2
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 732-594-1958
? TELEFAX: 732-594-4720
? TELEX:
? INFORMATION FOR SEQ ID NO: 10:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 346 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-09-828-432-3-10

```

```

Query March 12, 48; Score 259; EP 4; Length 349;
Best local Similarity 28.38; Pred. No. 1.66 14;
Matches 87, Conservative 54, Mismatches 109, Idols 19, Gaps 14.

QY 36 VGFVGNLCVIGLLHNAAKKEF EMHSLINSTATGILLFSAFIPATATSPSWALG 64
Db 36 VGFVGNLCVIGLLHNAAKKEF EMHSLINSTATGILLFSAFIPATATSPSWALG 64
QY 40 NUTLNSLITVLASEE EHEESTLILHLUSLALALILSIFECATVAGLTKWL 104
Db 40 NUTLNSLITVLASEE EHEESTLILHLUSLALALILSIFECATVAGLTKWL 104
QY 90 WPFVPSFPIHFMMAFSLITVVAFTFMAVSPATVSI-HRYTNSLVVA 140
Db 90 WPFVPSFPIHFMMAFSLITVVAFTFMAVSPATVSI-HRYTNSLVVA 140
QY 105 AFICK-----PIH-----VFPTVMGLVITFLAAMSTRTVAIVHSPFSSIVCPNALG 155
Db 105 AFICK-----PIH-----VFPTVMGLVITFLAAMSTRTVAIVHSPFSSIVCPNALG 155
QY 148 ----INTVASLLPPEFFSTIRHGEVE-MCLVDVPAVAEEFMSMEGLYEL--LARG 199
Db 148 ----INTVASLLPPEFFSTIRHGEVE-MCLVDVPAVAEEFMSMEGLYEL--LARG 199
QY 190 VGRWALSANAGFVAHGLKELHLNQLTQWEGW DELHFAVYVETVEGL 209
Db 190 VGRWALSANAGFVAHGLKELHLNQLTQWEGW DELHFAVYVETVEGL 209
QY 200 LPEFAFVFWMAVAGCEKELKELKELKELKELKELKELKELKELKELKELKEL 249
Db 200 LPEFAFVFWMAVAGCEKELKELKELKELKELKELKELKELKELKELKELKEL 249
QY 210 LPLLLCPYAVKLIHLHF LFMSAPFASVFFATLVVVVVVFS-SNLIHVVHLK 268
Db 210 LPLLLCPYAVKLIHLHF LFMSAPFASVFFATLVVVVVVFS-SNLIHVVHLK 268
QY 260 VHLKAAGAPPGGFI ALSQVLMSSISAMLLILVNSFFEP LKPVWFWMTTFPP 317
Db 260 VHLKAAGAPPGGFI ALSQVLMSSISAMLLILVNSFFEP LKPVWFWMTTFPP 317
QY 318 TVSESG 324
Db 318 TVSESG 324
QY 327 R-SETRE 332
Db 327 R-SETRE 332

RESULT 10
US-09-828-432-3
Sequence 2, Application US/098406508
Patent No. 639325
GENERAL INFORMATION:
APPLICANT: HINUMA, Shuji
APPLICANT: FUJII, Ryo
APPLICANT: FUKUSUMI, Shoji
APPLICANT: OHTAKI, Tetsuya
APPLICANT: HOSoya, Masaki
APPLICANT: HOSOI, Kazuhiko
APPLICANT: ONDA, Haruo
TITLE OF INVENTION: CALAMIN EFFECTIVE IN THE PREVENTION AND TREATMENT OF
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET

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? CITY: BOSTON
? STATE: MA
? COUNTRY: US
? ZIP: 02109
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FastSeq Version 1.5
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: 98/033,424B
? FILING DATE: 11-OCT-1995
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 7,134,412
? FILING DATE: 31-MAY-1995
? APPLICATION NUMBER: 6,126,610
? FILING DATE: 28-DEC-1994
? APPLICATION NUMBER: 6,247,599
? FILING DATE: 13-OCT-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: RESNICK, DAVID S.
? REGISTRATION NUMBER: 34,335
? REFERENCE/COCKET NUMBER: 45901
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 617-523-3400
? TELEFAX: 617-523-6440
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 148
? TYPE: Amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: Peptide
? US-09-828-432-3-2

Query March 12, 48; Score 269; EP 4; Length 349;
Best local Similarity 28.38; Pred. No. 1.66 14;
Matches 87, Conservative 54, Mismatches 109, Idols 19, Gaps 14.

QY 36 VGFVGNLCVIGLLHNAAKKEF EMHSLINSTATGILLFSAFIPATATSPSWALG 64
Db 36 VGFVGNLCVIGLLHNAAKKEF EMHSLINSTATGILLFSAFIPATATSPSWALG 64
QY 40 NUTLNSLITVLASEE EHEESTLILHLUSLALALILSIFECATVAGLTKWL 104
Db 40 NUTLNSLITVLASEE EHEESTLILHLUSLALALILSIFECATVAGLTKWL 104
QY 90 WPFVPSFPIHFMMAFSLITVVAFTFMAVSPATVSI-HRYTNSLVVA 140
Db 90 WPFVPSFPIHFMMAFSLITVVAFTFMAVSPATVSI-HRYTNSLVVA 140
QY 105 AFICK-----PIH-----VFPTVMGLVITFLAAMSTRTVAIVHSPFSSIVCPNALG 155
Db 105 AFICK-----PIH-----VFPTVMGLVITFLAAMSTRTVAIVHSPFSSIVCPNALG 155
QY 148 ----INTVASLLPPEFFSTIRHGEVE-MCLVDVPAVAEEFMSMEGLYEL--LARG 199
Db 148 ----INTVASLLPPEFFSTIRHGEVE-MCLVDVPAVAEEFMSMEGLYEL--LARG 199
QY 190 VGRWALSANAGFVAHGLKELHLNQLTQWEGW DELHFAVYVETVEGL 209
Db 190 VGRWALSANAGFVAHGLKELHLNQLTQWEGW DELHFAVYVETVEGL 209
QY 200 LPEFAFVFWMAVAGCEKELKELKELKELKELKELKELKELKELKELKELKEL 249
Db 200 LPEFAFVFWMAVAGCEKELKELKELKELKELKELKELKELKELKELKELKEL 249
QY 210 LPLLLCPYAVKLIHLHF LFMSAPFASVFFATLVVVVVVFS-SNLIHVVHLK 268
Db 210 LPLLLCPYAVKLIHLHF LFMSAPFASVFFATLVVVVVVFS-SNLIHVVHLK 268
QY 260 VHLKAAGAPPGGFI ALSQVLMSSISAMLLILVNSFFEP LKPVWFWMTTFPP 317
Db 260 VHLKAAGAPPGGFI ALSQVLMSSISAMLLILVNSFFEP LKPVWFWMTTFPP 317
QY 318 TVSESG 324
Db 318 TVSESG 324
QY 327 R-SETRE 332
Db 327 R-SETRE 332

RESULT 11
US-09-828-432-3
Sequence 2, Application US/098406508
Patent No. 6114139
GENERAL INFORMATION:
APPLICANT: HINUMA, Shuji
APPLICANT: HOSoya, Masaki
APPLICANT: FUJII, Ryo
APPLICANT: OHTAKI, Tetsuya

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Db 181 VAEFMSMFKYLPVLLAPLPLPFASFYFWPAYDQCYFPTTQNLPNQIPSKQVTVMLL 240
QY 241 SIATISALLMLPEWVAWLWWHLKAAAGAPPQGFIALGVLMFGSSANPLIFLWSEEF 300
Db 241 SIATISALLMLPEWVAWLWWHLKAAAGAPPQGFIALGVLMFGSSANPLIFLWSEEF 300
QY 301 PEGIKGVWMMITKYPPTVSESQETPAGNSGLPDPVPSPPSPASIPPEKSSSSSSGK 360
Db 301 PEGIKGVWMMITKYPPTVSESQETPAGNSGLPDPVPSPPSPASIPPEKSSSSSSGK 360
QY 361 KTEKAEIPIIPDVEQFWHERDTVPSCQNDPDPWFHEDTETEGV 400
Db 361 KTEKAEIPIIPDVEQFWHERDTVPSCQNDPDPWFHEDTETEGV 400

```

RESULT 2

US-09-766-693-2

Sequence 2, Application US/09766693

Parent No. US2001001633A1

GENERAL INFORMATION:

APPLICANT: ELISHOURBAGY, NABIL
 APPLICANT: MICHALOVICH, DAVID
 APPLICANT: SHABON, USMAN
 TITLE OF INVENTION: MOLECULAR CLONING OF A GALANIN LIKE 7TM
 TITLE OF INVENTION: RECEPTOR (AXOR40)

FILE REFERENCE: GP-70649-C1

CURRENT APPLICATION NUMBER: US/09/766,693

PRIOR FILING DATE: 2001-01-22

PRIOR FILING DATE: 1999-10-12

PRIOR APPLICATION NUMBER: UK 9920168 3

PRIOR FILING DATE: 1999-08-24

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 2

LENGTH: 419

TYPE: PRT

ORGANISM: HOMO SAPIENS

US-09-766-693-2

Query Match 100.0%; Score 2167; DB 10; Length 419;
 Best Local Similarity 100.0%; Field No. 46-176;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MNVSFAHLHFAGGYLPSDSQWRTIIPALLVAVLVGVNLCVIGILLHNAAWKGPSMI 60
Db 14 MNVSFAHLHFAGGYLPSDSQWRTIIPALLVAVLVGVNLCVIGILLHNAAWKGPSMI 73
QY 61 HSLILNLSLADLSLLPSAPITATAYKSWDLGWFWCKSSDWFIHTCMAAKSLTIIVVA 120
Db 74 HSLILNLSLADLSLLPSAPITATAYKSWDLGWFWCKSSDWFIHTCMAAKSLTIIVVA 133
QY 121 KVCFTYASDPAKQVSHNYTIWVLAIVTVAISLLPDPFWFFSTPHHGVEMCLVDVPA 180
Db 134 KVCFTYASDPAKQVSHNYTIWVLAIVTVAISLLPDPFWFFSTPHHGVEMCLVDVPA 193
QY 181 VAEFMSMFKYLPVLLAPLPLPFASFYFWPAYDQCYFPTTQNLPNQIPSKQVTVMLL 240
Db 194 VAEFMSMFKYLPVLLAPLPLPFASFYFWPAYDQCYFPTTQNLPNQIPSKQVTVMLL 253
QY 241 SIATISALLMLPEWVAWLWWHLKAAAGAPPQGFIALGVLMFGSSANPLIFLWSEEF 300
Db 254 SIATISALLMLPEWVAWLWWHLKAAAGAPPQGFIALGVLMFGSSANPLIFLWSEEF 313
QY 301 PEGIKGVWMMITKYPPTVSESQETPAGNSGLPDPVPSPPSPASIPPEKSSSSSSGK 360
Db 314 PEGIKGVWMMITKYPPTVSESQETPAGNSGLPDPVPSPPSPASIPPEKSSSSSSGK 372
QY 361 KTEKAEIPIIPDVEQFWHERDTVPSCQNDPDPWFHEDTETEGV 400
Db 374 KTEKAEIPIIPDVEQFWHERDTVPSCQNDPDPWFHEDTETEGV 419

```

RESULT 3

US-09-828-432-2

Sequence 2, Application US/09828432

Parent No. US20020137132A1

GENERAL INFORMATION:

APPLICANT: Vogeli, Gabriel
 APPLICANT: Lind, Peter
 APPLICANT: Sejlitz, Torsten
 APPLICANT: Berthold, Malin
 TITLE OF INVENTION: G Protein coupled receptors
 FILE REFERENCE: 00145-US1

CURRENT APPLICATION NUMBER: US/09/828,432

PRIOR FILING DATE: 2001-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR APPLICATION NUMBER: 60/251,113

PRIOR FILING DATE: 2000-12-05

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patent'n version 3.0

SEQ ID NO 2

LENGTH: 419

TYPE: PRT

ORGANISM: Homo sapiens

US 09 828-432-2

Query Match 100.0%; Score 2167; DB 10; Length 419;

Best Local Similarity 100.0%; Field No. 2-46-176;

Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MNVSFAHLHFAGGYLPSDSQWRTIIPALLVAVLVGVNLCVIGILLHNAAWKGPSMI 60
Db 14 MNVSFAHLHFAGGYLPSDSQWRTIIPALLVAVLVGVNLCVIGILLHNAAWKGPSMI 73
QY 61 HSLILNLSLADLSLLPSAPITATAYKSWDLGWFWCKSSDWFIHTCMAAKSLTIIVVA 120
Db 74 HSLILNLSLADLSLLPSAPITATAYKSWDLGWFWCKSSDWFIHTCMAAKSLTIIVVA 133
QY 121 KVCFTYASDPAKQVSHNYTIWVLAIVTVAISLLPDPFWFFSTPHHGVEMCLVDVPA 180
Db 134 KVCFTYASDPAKQVSHNYTIWVLAIVTVAISLLPDPFWFFSTPHHGVEMCLVDVPA 193
QY 181 VAEFMSMFKYLPVLLAPLPLPFASFYFWPAYDQCYFPTTQNLPNQIPSKQVTVMLL 240
Db 194 VAEFMSMFKYLPVLLAPLPLPFASFYFWPAYDQCYFPTTQNLPNQIPSKQVTVMLL 253
QY 241 SIATISALLMLPEWVAWLWWHLKAAAGAPPQGFIALGVLMFGSSANPLIFLWSEEF 300
Db 254 SIATISALLMLPEWVAWLWWHLKAAAGAPPQGFIALGVLMFGSSANPLIFLWSEEF 313
QY 301 PEGIKGVWMMITKYPPTVSESQETPAGNSGLPDPVPSPPSPASIPPEKSSSSSSGK 360
Db 314 PEGIKGVWMMITKYPPTVSESQETPAGNSGLPDPVPSPPSPASIPPEKSSSSSSGK 372
QY 361 KTEKAEIPIIPDVEQFWHERDTVPSCQNDPDPWFHEDTETEGV 400
Db 374 KTEKAEIPIIPDVEQFWHERDTVPSCQNDPDPWFHEDTETEGV 419

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RESULT 4

US-10-040-960-5

Sequence 5, Application US/10080960

Publication No. US20020197696A1

GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc.
 APPLICANT: Glucksmann, Maria
 APPLICANT: Meyers, Rachel

TITLE OF INVENTION: R0002, 12074, 12080, 03497, AND 4443

TITLE OF INVENTION: NETHOS AND COMBINATIONS THEREOF

FILE REFERENCE: 3618, 20044, 00

CURRENT APPLICATION NUMBER: US/10/080,960

PRIOR FILING DATE: 2001-10-19

PRIOR APPLICATION NUMBER: US 60/242,040

; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: US 60/242,039
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: US 60/241,992
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: US 60/242,637
 ; PRIOR FILING DATE: 2000-10-20
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 461
 ; TYPE: PPT
 ; ORGANISM: Homo sapiens
 ; US-10-080-960-5

Query Match 94.9% Score 2055, 28 1, Length 461.
 Best Local Similarity 100.0%; Pred. No. 8, 76-167; Gaps 0;
 Matches 387; Conservative 0; Mismatches 0; Indels 0;
 QY 1 MMSVFAHLHFAAGYLPSQDWTTFIALLVAVTVGVENLVISILHRAWGPFSSMI 40
 DB 1 MMSVFAHLHFAAGYLPSQDWTTFIALLVAVTVGVENLVISILHRAWGPFSSMI 40
 QY 61 HSLIINLSLADLSLLFAPAPATATAYSSVMDI GMPVYFSSDWFHTTMAAFPSITIVVVA 100
 DB 61 HSLIINLSLADLSLLFAPAPATATAYSSVMDI GMPVYFSSDWFHTTMAAFPSITIVVVA 100
 QY 121 KVCNMYASDPKQVSIHNTVMSVVAIWTVASLLPLFEMPFSTIRHHEGVEMCLVDVFA 180
 DB 121 KVCNMYASDPKQVSIHNTVMSVVAIWTVASLLPLFEMPFSTIRHHEGVEMCLVDVFA 180
 QY 181 VAEERMSMGKLYPLLAFLGLPLFPFASFPWPAYDQYFRTQNLPHQIPSKQVTVMLL 240
 DB 181 VAEERMSMGKLYPLLAFLGLPLFPFASFPWPAYDQYFRTQNLPHQIPSKQVTVMLL 240
 QY 241 STAIISALLWIDENWAWLWHLKKAAGAPPQCFIALSQVLMFSSISSANPLIFLMSSEF 300
 DB 241 STAIISALLWIDENWAWLWHLKKAAGAPPQCFIALSQVLMFSSISSANPLIFLMSSEF 300
 QY 301 KTEKAEIRIPEDVEGFWHERDTPSVQ 387
 DB 301 KTEKAEIRIPEDVEGFWHERDTPSVQ 387

RESULT 5
 US-10-090-569-2
 ; Sequence 5, Application US/10090569
 ; Publication No. US2003000829A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HINUMA, Shuji
 ; FUJII, Ryo
 ; FUKUSUMI, Shoji
 ; OHTAKI, Tetsuya
 ; HOSOYA, Masaki
 ; OHGI, Kazuhiro
 ; ONDA, Haruo
 ; TITLE OF INVENTION: GALANIN RECEPTOR PROTEIN, PRODUCTION AND USE THEREOF
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DIFF. PRONSTEIN, ROBERTS & CUSHMAN
 ; STREET: 130 WATER STREET
 ; CITY: POSTON
 ; STATE: MA
 ; COUNTRY: US
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10090569
 ; FILING DATE: 04-Mar-2002
 ; CLASSIFICATION: <Unknown>
 ; FEIC APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/540,650
 ; FILING DATE: 11-OCT-1995
 ; APPLICATION NUMBER: 7-134412
 ; FILING DATE: 31-MAY-1995
 ; APPLICATION NUMBER: 6-326610
 ; FILING DATE: 28-DEC-1994
 ; APPLICATION NUMBER: 6-247599
 ; FILING DATE: 13-OCT-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: RESNICK, DAVID S.
 ; REGISTRATION NUMBER: 34,235
 ; REFERENCE/DOCKET NUMBER: 45001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-523-3400
 ; TELEFAX: 617-523-6440
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 348
 ; TYPE: Amino acid
 ; TOPOLOGY: Linear
 ; MOLECULE TYPE: Peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 ; US-10-090-569-2

Query Match 12.4%; Score 269; DB 9; Length 348;
 Best Local Similarity 28.3%; Pred. No. 2, 16-10;
 Matches 87; Conservative 54; Mismatches 128; Indels 14;
 QY 36 VGVNGLCHGLLHRAWKPK-SMTHGLIINLSLADLSLLFCAICARATAY-KETWGL 14
 DB 46 MGVNGLSLVTVAFK-PKPFSTIRHHEGVEMCLVDVFA 104
 QY 95 WPVYSSDPKQVSIHNTVMSVVAIWTVASDPKQVSIHNTVMSVVA 14
 DB 105 APTK----PIH-----YPTVSMVLSIFTLAASVDPVVAIVHSEPSLSISNAL 184
 QY 148 ---IWTVASLLPLFEMPFSTIRHHEGVEMCLVDVFAVAEERMSMGKLYPL 180
 DB 156 VGFPTWALSIAVASPVAYHGLPHRDSNQTFCWEQW-----NELHKAAYVAIVTEGVL 200
 QY 200 LPLFPEASEVENAYDCKKFGFTQNLPHQIPSKQVTVMLLSTAIISALLWIDENWAWL 160
 DB 210 LPLLLICFYAPVYHILHPL LPMSPFSEACPFYACQVTVTVTVTGILWIDENWAWL 246
 QY 260 VMLHFAASAPFSSFI-ALSLVMSISGANPLIFLMSSEPSISSANPLIFLMSSEF 117
 DB 260 AEP GAPPTWASPPFPIAH-LATNSVHRIIVAPICRSPKAYVIVHRAWTEH 206
 QY 318 TVSESQE 324
 DB 327 P-SETYE 332

RESULT 6
 US-10-090-569-5
 ; Sequence 5, Application US/10090569
 ; Publication No. US2003000829A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HINUMA, Shuji
 ; FUJII, Ryo
 ; FUKUSUMI, Shoji
 ; OHTAKI, Tetsuya
 ; HOSOYA, Masaki
 ; OHGI, Kazuhiro
 ; ONDA, Haruo
 ; TITLE OF INVENTION: GALANIN RECEPTOR PROTEIN, PRODUCTION AND USE THEREOF
 ; NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS
 ADDRESSEE TYPE: REPRINTS, FORESTS & CUSHMAN
 STREET: 130 WATER STREET
 CITY: BOSTON
 STATE: MA
 COUNTRY: US

ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/02/090,569
 FILING DATE: 04-Mar-2002
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/540,650
 FILING DATE: 11-OCT-1995
 APPLICATION NUMBER: 7-134412
 FILING DATE: 31-MAY-1995
 APPLICATION NUMBER: 6-326610
 FILING DATE: 28-DEC-1994
 APPLICATION NUMBER: 6-247599
 FILING DATE: 13-OCT-1994

ATTORNEY/AGENT INFORMATION:
 NAME: PEGSNEY, DAVID S.
 REGISTRATION NUMBER: 34,235
 REFERENCE/DOCKET NUMBER: 459-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO. 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 449
 TYPE: Amino acid
 TOPOLOGY: Linear
 MOLECULE TYPE: Peptide
 SEQUENCE DESCRIPTION: SEQ ID NO. 5:
 US-10 090-569-5

Query Match 12.1%, Score 262.5, Db 9, Length 349;
 Best Local Similarity 26.8%, Pfad No. 7 40-15,
 Matches 88; Conservative 61, Mismatches 124, Indels 59, Gaps 16,

QY 36 VGFVGNLVGILLHNAWKGP-SMHSILNLNLADLSLLLESAPIRATAYSKSVNDLG 94
 Db 46 LGVIGNSLVITVLARK-PGRPESTNLNLFNLSTADLALYLCIPFQATVVALPTWVG 104
 QY 95 WFCVCKSDWFIHTCMAAKSLTIWVAKVCFMVASDPKQVSI-HNYTIWSVLVA----- 147
 Db 105 AFICK-----FIH-----YFETVSMVSVIETLAAMSVDPYVAIVHSPSSSLVSPNALIG 155
 QY 148 ---IWTVASLLPLPEWFFSTIRHGV-----EMCLVDVPVAEAEPMFMFGKLYPL- 195
 Db 156 VSGTMAISAMASG-----VATGTHIFHPPASNGTFTWELWPCPHK-----FAYVVV 203
 QY 196 ILEFFASVEWFAVGVYFSTCTCLPFLIPFVTVWVLSIALISALLWLP 242
 Db 204 TEVFGHLPLILICFYAVVNIHHTF-LNNMFYSEASFPPTATVTVVVVVFGLSWLP 267
 QY 293 EWVAWLWVWLKAAGPAPPGPI--ALSOVMFESISANFLPLVMSSEFFEGKGVWVW 310
 Db 263 HHIHWARP--GVFPLTPASLPPIAHCLAYSNSVNPIIYVLSNFRKAYKQVFK 320
 QY 311 MITYKPTVTSQRTACSGPLPKVVPSPES 342
 Db 301 HI FKHULSDTFKES PIDTTS 343

RESULT 7
 US-09-903-396A-2
 Sequence 2, Application US/00003306A

Publication No. US2002/0194657A1
 GENERAL INFORMATION:
 APPLICANT: Allen, Keith D.
 TITLE OF INVENTION: TRANSGENIC MICE CONTAINING
 TITLE OF INVENTION: GLUCOCORTICOID INDUCED REVERSE TRANSCRIPTION
 FILE REFERENCE: P-359
 CURRENT APPLICATION NUMBER: US/09/903,306A
 PRIOR FILING DATE: 2002-07-15
 PRIOR APPLICATION NUMBER: US 60/217,179
 PRIOR FILING DATE: 2000-07-10
 PRIOR APPLICATION NUMBER: US 60/252,299
 PRIOR FILING DATE: 2000-11-20
 PRIOR APPLICATION NUMBER: US 60/284,205
 PRIOR FILING DATE: 2001-01-15
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 423
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-903-396A-2

Query Match 10.0%, Score 294.5, Db 9, Length 473;
 Best Local Similarity 24.5%, Pfad No. 1 156-127,
 Matches 101; Conservative 60, Mismatches 174, Indels 100, Gaps 100

QY 6 AHLHFAGSYLISQEW PTFIALVA VLVYFQNFVNDLILH 100
 Db 39 ASSHEWARYTFSEWNEVFYFVCAEDNTVPALEIVAVFVTVQVQVYVQWVWV 94
 QY 51 NAWKGRKSMHS-----LILNLSLALLESAPIRATAYSKSVNDLG 104
 Db 29 N-----QPMHSATLIVLAVAGNITLITFLVLCVTSQV-KVWVWVWV 152
 QY 107 TQMAAKSLTIWVAKVCFMVASDPKQVSI-HNYTIWSVLVA----- 147
 Db 153 CSLHVSALTITAIATVGRH-VIMHPIKPEIETIKGVIV IAVWVWVWVWVWV 190
 QY 163 STIRHGV EMCLVDVPVAEAEPMFMFGKLYPL- 195
 Db 211 PTFYSEDIVRSCLPFPFPAFLPFWYHATFILLHCLPFLVAVFVAVFVAVFV 200
 QY 214 YPR-TTTPHPSLPEFVTVWVLSIALISALLWLP 242
 Db 271 TIGEVTEGVLAIRPEKTYTVMIVLVVLEALWEP INAVVWVWVWVWV 247
 QY 276 ALSCLVLP-----GLSSANLIFLMSSEFFEGKGVWVWVWVWVWVWV 310
 Db 321 HTNNAFYAFIHWFAMSTCYNFIYCWNIHNPVRLKAL 320
 QY 329 NSESLFPVF SFGHSHHFFKFGSGKRLKALI PII 370
 Db 370 QEDLPSPVSPFVWVTEKSHSPAPFNHULSSSLV 370

RESULT 8

US-10-029-009-9
 Sequence 3, Application US/02/090,569
 Patent No. US2002/016417A1
 GENERAL INFORMATION:
 APPLICANT: Felsch, Jason S.
 APPLICANT: Amis, David Allen
 APPLICANT: Kalghargi, Krishna
 APPLICANT: Nash, Huw M.
 TITLE OF INVENTION: Affinity Selection Based Sequencing of Hybridoma Cell Lines
 FILE REFERENCE: 11035173 US2
 CURRENT APPLICATION NUMBER: US/10/629,009
 CURRENT FILING DATE: 2002-03-28
 PRIOR APPLICATION NUMBER: US 60/258,970
 PRIOR FILING DATE: 2000-12-29
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 9

LENGTH: 488
TYPE: PRT
ORGANISM: Human
US-10-029-009-9

Query Match 1038; Score 224; DB 9; Length 488;
Best Local Similarity 23.68; Pred. No. 3 de-11;
Matches 78; Conservative 62; Mismatches 133; Indels 58; Gaps 12;

QY 16 PSDQDWTII-----PALLVA-----VCLVGFVNCVLCVIGILLRNWKFSPSHRS 62
DB 65 PAPQPMWNTNQVQVQVFWPRLALSLAVGVVAVAVAGSLVIMIL AHPKMTVTHY 102
QY 63 LILNLSADLSLLPSADIPATAVSKVMDLQWVCKSSDWFHTCMAAKSLTIWVAVK 102
DB 130 FLVNLAFDASMAAPNTVNIYVILHSWYFGAHYCRCPPTITAVPASVYSTAINT 199
QY 123 CPWVASDPAK QVSHNYITNSVVAIVTASLLPLPEWFSTIRHIEGVCMCLVDVPAV 181
DB 183 PYMATIDPKPLKATATKI--VIGSIWILAFLLAPQCHYSKTKVMPGPTLCFVQWPEG 240
QY 192 ABEEMS-----MEGKLYPLLAFGLPLFFASFPYFPAV--DQVYKPGTGTQNI:PHOIFS 210
DB 241 PCHFTTHIIVILVYFHLIMGITYIVITVILWSEHLPQETLDE-----NHEQLFA 233
QY 233 KQVTVMLLSIAIS--ALLWLPBW-----AWLWVHLKAAAGPAPPGQFIALSQ 279
DB 294 PKVVMVMIIVMTFAICWLPYHIVIFULTAIYQCLNPKYI-----QQVYLA SF 342
QY 280 VIMPSISSANPLIFVMSEEPFEGIKGVWKK 310
DB 343 WLAMSTMYNPIIYCCLNPPFPAGFPAPPW 373

RESULT 9

US-10-029-009-21
Sequence 21, Application US/10029009
Patent No. US2002064617A1
GENERAL INFORMATION:
APPLICANT: Felsch, Jason S.
APPLICANT: Annis, David Allen
APPLICANT: Kalghatgi, Krishna
APPLICANT: Nash, Huw M.
TITLE OF INVENTION: Affinity Selection-Based Screening of Hydrophobic Proteins
FILE REFERENCE: 111025 173 US2
CURRENT APPLICATION NUMBER: US/10/029,609
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/258,970
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 505
TYPE: PRT
ORGANISM: Human
US-10-029-009-21

Query Match 1038; Score 224; DB 9; Length 505;
Best Local Similarity 23.68; Pred. No. 3 de-11;
Matches 78; Conservative 62; Mismatches 133; Indels 58; Gaps 12;

QY 16 PSDQDWTII-----PALLVA-----VCLVGFVNCVLCVIGILLRNWKFSPSHRS 62
DB 81 PAPQPMWNTNQVQVQVFWPRLALSLAVGVVAVAVAGSLVIMIL AHPKMTVTHY 129
QY 63 LILNLSADLSLLPSADIPATAVSKVMDLQWVCKSSDWFHTCMAAKSLTIWVAVK 122
DB 130 FLVNLAFDASMAAPNTVNIYVILHSWYFGAHYCRCPPTITAVPASVYSTAINT 199
QY 123 CPWVASDPAK QVSHNYITNSVVAIVTASLLPLPEWFSTIRHIEGVCMCLVDVPAV 181
DB 183 PYMATIDPKPLKATATKI--VIGSIWILAFLLAPQCHYSKTKVMPGPTLCFVQWPEG 240

QY 192 ABEEMS-----MEGKLYPLLAFGLPLFFASFPYFPAV--DQVYKPGTGTQNI:PHOIFS 210
DB 257 PKCHFTTHIIVILVYFHLIMGITYIVITVILWSEHLPQETLDE-----NHEQLFA 109
QY 233 KQVTVMLLSIAIS--ALLWLPBW-----AWLWVHLKAAAGPAPPGQFIALSQ 279
DB 294 PKVVMVMIIVMTFAICWLPYHIVIFULTAIYQCLNPKYI-----QQVYLA SF 342
QY 280 VIMPSISSANPLIFVMSEEPFEGIKGVWKK 310
DB 359 WLAMSTMYNPIIYCCLNPPFPAGFPAPPW 389

RESULT 10

US-08-796-570A-1
Sequence 1, Application US/08-796-570A
Patent No. US20020009771A1
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: G Protein-Coupled Receptor Proteins,
METHOD OF INVENTION: Their Production And Use
NUMBER OF SEQUENCES: 19
CURRENT INVENTOR'S ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/796,570A
FILING DATE: 06-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: Japan 8-021562
FILING DATE: 2-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald I.
REGISTRATION NUMBER: 30,628
REFERENCE/DOCKET NUMBER: 47147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 423
TYPE: Amino acid
LOGOLOGY: Linear
MOLECULE TYPE: Peptide
US-08-796-570A-1

Query Match 9.93; Score 215.5; DB 9; Length 423;
Best Local Similarity 22.23; Pred. No. 3 de-11;
Matches 95; Conservative 65; Mismatches 153; Indels 153; Gaps 18;

QY 6 AMHLPAGGHTGSLFQW-----KLLIALLVA YQNGVYVNLVIGILLRNW 50
DB 39 SHFFQNMNTTQVNFVGPFPYDAESQHTVALLIVAYGFTIVELFQNMVYVYK 94
QY 51 NAWKGFSLHG-----LILNLSADLSLLPSADIPATAVSKVMDLQWVCKSSDWF 106
DB 99 H-----QNHGATSLFVRLAVAGIMILMTFTLTFFSTWTFHKNCHVNEAT 182
QY 107 TCMAKSLTIWVAVKVPWYASDFAP QVSHNYITNSVVAIVTASLLPLPEWF--F 162
DB 153 QSHVSAHITAIADVPHQVIMPLKPLPRTITPQNIY IAVINWVATFSLDHALQK 110

Db 145 NPTGWPFFISQAYLGIYLIWVIACVLSLFLANSILENVFHKHKALEP-LADKVVCTE 203
 QY 184 EF-----MSMEGLYPLLAFLGLPFEASPYFWAYDQCKZCTKTONTLBNIPS---KOV 235
 Db 204 SWPLAHPHTIYTTLLILQYQYPLUGFIIIVGVAPIYVPLQQRQVPHFHTYSLPASHWQV 263
 QY 236 TWMLLSIAIISALLWPEWV AMLVWHLKAGAPAPQGFIALSQVLMFSISSANPLFLV 294
 Db 264 NVVLVGVVAVAPVLMPLHVSLESDWHEAIFICHGNIIFLVCHLLAMASTGVNFYIYG 323
 QY 205 VNCSEPPFGLKVVWVWVTVYPTTUSEQPTPAKNSGEP 334
 Db 324 FLNTNFKYEIKAL-----VLTCQOSAPLESEHLP 353

RESULT 13
 US-09-292-973-19
 ; Sequence 19, Application US/09292973
 ; Patent No. US20020111473A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ZAGTAWNY, Roman L.
 ; TITLE OF INVENTION: NO. US20020111473A1:el G Protein Coupled Receptor
 ; FILE REFERENCE: 9074-9004
 ; CURRENT APPLICATION NUMBER: US/09/292-973
 ; EARLIER FILING DATE: 1998-04-16
 ; EARLIER FILING DATE: 1998-04-16
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 19
 ; LENGTH: 426
 ; TYPE: PRT
 ; ORGANISM: Rattus sp
 ; US-09-292-973-19

Query Match 9.5%; Score 205.5; DB 10; Length 426;
 Best Local Similarity 24.5%; Pred. No. 6,7e-10;
 Matches 91; Conservative 54; Mismatches 170; Indels 57; Gaps 13;
 QY 28 ALLVAVCLVGVNLCVIGILLHNAWKQKPSMIHSLIINLSLADLSLLESAPIRATAYS 87
 Db 48 AAVVLIPLCVNTLVYFIVLKN FHMFTVTRNFMFLHVAQDCLVIFCMFTLLVDNL 105
 QY 88 KSVMDLGNFVCKSSDWFHTTMAAKSLTIWVAVKVFMYACDPAPQVGHNTYIMSVLVA 147
 Db 106 ITCMPDNATCKMSGLVQMSVSASVFTLVAIVERFPCIVHPPEKLTLEKALFTIAV 164
 QY 148 INTVASLLPLPEWFFSTI---RHHEGVNCLVDVPAVAEEFMSMGF-----KLYPLL 196
 Db 165 IVALALLMCPSSAVTLTVTFEEHH-----FMLDAPNPSYPLYSWGAWPEKMEKAVITAV 213
 QY 197 AFG---LPLFEASFYEWFAVQCKKFG---TPTCNLSNCHIESQVTVMLLSIAI 244
 Db 220 LPAHYIVPLALIVVMYVPIAPVLCQAPGAPDTEFAVAGOPTSPBPAPVVMIAWVAL 279
 QY 245 ICAALLWLEFWAWLVWV---WHKKAAGAPAPQGFIALSQVLMFSISSANPLFLV 295
 Db 280 FPTLSMFLWVLLIDYGEISELQHLHLSVAVP-----LAHMLAFPHSSANPLIYGY 323
 QY 296 MKEEPFEGKGVWV---KMTFFPTVTSSECTPAKNSGCLPTFPVPSFSP--ASIEPK 349
 Db 334 FNEHFFPGGCAAFACQIWTW-----PFWAAHPQAYSEPPNPLLPVWVTVVQPSGLPSF 388
 QY 350 EKPSSSPSSGKGV 361
 Db 389 GPPSSGVPGPGR 400

RESULT 14
 US-09-292-973-2
 ; Sequence 2, Application US/09292973
 ; Patent No. US20020111473A1

GENERAL INFORMATION:
 ; APPLICANT: ZAGTAWNY, Roman L.
 ; TITLE OF INVENTION: NO. US20020111473A1:el G Protein Coupled Receptor
 ; FILE REFERENCE: 9074-9004
 ; CURRENT APPLICATION NUMBER: US/09/292-973
 ; EARLIER FILING DATE: 1998-04-16
 ; EARLIER FILING DATE: 1998-04-16
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 432
 ; TYPE: PRT
 ; ORGANISM: Rattus sp.
 ; US-09-292-973-2

Query Match 9.5%; Score 205.5; DB 10; Length 432;
 Best Local Similarity 24.5%; Pred. No. 6,7e-10;
 Matches 91; Conservative 54; Mismatches 170; Indels 57; Gaps 13;
 QY 29 ALLVAVCLVGVNLCVIGILLHNAWKQKPSMIHSLIINLSLADLSLLESAPIRATAYS 87
 Db 48 AAVVLIPLCVNTLVYFIVLKN FHMFTVTRNFMFLHVAQDCLVIFCMFTLLVDNL 105
 QY 88 KSVMDLGNFVCKSSDWFHTTMAAKSLTIWVAVKVFMYACDPAPQVGHNTYIMSVLVA 147
 Db 106 ITCMPDNATCKMSGLVQMSVSASVFTLVAIVERFPCIVHPPEKLTLEKALFTIAV 164
 QY 148 INTVASLLPLPEWFFSTI---RHHEGVNCLVDVPAVAEEFMSMGF-----KLYPLL 196
 Db 165 IVALALLMCPSSAVTLTVTFEEHH-----FMLDAPNPSYPLYSWGAWPEKMEKAVITAV 213
 QY 197 AFG---LPLFEASFYEWFAVQCKKFG---TPTCNLSNCHIESQVTVMLLSIAI 244
 Db 220 LPAHYIVPLALIVVMYVPIAPVLCQAPGAPDTEFAVAGOPTSPBPAPVVMIAWVAL 279
 QY 245 ICAALLWLEFWAWLVWV---WHKKAAGAPAPQGFIALSQVLMFSISSANPLFLV 295
 Db 280 FPTLSMFLWVLLIDYGEISELQHLHLSVAVP-----LAHMLAFPHSSANPLIYGY 323
 QY 296 MKEEPFEGKGVWV---KMTFFPTVTSSECTPAKNSGCLPTFPVPSFSP--ASIEPK 349
 Db 334 FNEHFFPGGCAAFACQIWTW-----PFWAAHPQAYSEPPNPLLPVWVTVVQPSGLPSF 388
 QY 350 EKPSSSPSSGKGV 361
 Db 389 GPPSSGVPGPGR 400

RESULT 15
 US-10-112-599A-2
 ; Sequence 2, Application US/10112599A
 ; Publication No. US20010005476A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Allen, Keith D.
 ; TITLE OF INVENTION: ELISA-CPITID-PEPTIDE IDENTIFICATION,
 ; FILE REFERENCE: P-678
 ; CURRENT APPLICATION NUMBER: US/10/112,599A
 ; CURRENT FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/290,513
 ; PRIOR FILING DATE: 2001-03-29
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PartSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 372
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-10-112-599A-2

Query Match 9.4%; Score 203.5; DB 9; Length 372;
 Best Local Similarity 23.8%; Pred. No. 8,1e-10;

